## SEARCH REQUEST FORM

Scientific and Technical Information Center

· (.	Peline Gian	
Requester's Full Name: 03/	515363	Examiner # : _ 78710 Date: 1/26/05 7 Serial Number: 09/5/3363
Art Unit: 1636 Phone	Number $\frac{30}{2} = 0.77$	7 Serial Number: 09/5/3363
		esults Format Preferred (circle): APER DISK E-MAIL
If more than one search is sub	mitted, please priori	tize searches in order of need. 09/515363
Please provide a detailed statement of t	he search topic, and describ	be as specifically as possible the subject matter to be searched.
	ns that may have a special i	conyms, and registry numbers, and combine with the concept or meaning. Give examples or relevant citations, authors, etc. if additional abstract.
Title of Invention: Melanon	na differents	ation associated Bene-5, Promoter & uses
Inventors (please provide full names)		
		CRFE
Earliest Priority Filing Date:	معمد د / فحد ا	
	• •	n (parent, child, divisional, or issued patent numbers) along with the
appropriate serial number.	une un perimeni injurmatar	n (parem, ema, arossana, az issaeu parem namners) mang wita me
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uic Searcher Picked Up / 26/05	Bibliographic	Dr.Link
ate Completed/ JOHN S	Litigation	Lexis/Nexis
archer Pref Review Time	Folliest	Sequence Systems Q6P/Q2P
crical Prepares.	Patent Family	WWW/Internet
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2341 ACAAAAACACGACAGAGTGCATATGCGCTTTCCCAGTGGATTACTGAAAATGAAAATTT 2400 	AGAAATACCATAATGGAGCAATATATACTAGGACTGAGGAATCAGCACGAGGAATAATCTTT AGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCAGCACGAGGAATAATCTTT			2101 ACIGAICANGAGIGAIGA GAIGAGIA I ICIGAIGAGAGA ICAAGAICAAGAICAAGAI I AAAG 2100	CATCITIGAAACITTCTAFAATGAAGAGAAAGATAAGAACITTGCACCATCATAGAAGATGAT	AGGAAGTACAATGAGGCCCTACAAATTAATGACACAATTCGAATGATAGATGCGTATACT 	ATGGAAAAAAAGCTGCAAAAAAAGGAAATCGCAAAGAAGGTGTTTGTGCAGAACATTTG	TGTCAAATGAGTCCAATGTCAGATTTTGGAACTCAACCCTATGAACAATGGGCCATTCAA		CTTGATCAACTGAAAAACCAAATTCAGGAGCCATGCAAGAAGTTTGCCATTGCAGATGCA		CTGGGACTAACAGCTTCACCTGGTGTTGGAGGGCCCACGAAGCCCAAGCCCAAGCAGAGACAAGCTGAAGAA			141 GAAAATGGAGAAGATGCTGGTGTCAATTGTCAGCTTTTCCCCCATTATCATTGATGAA 1500 		TATCGTGTTATTGGATTAAGTGGTGATACCCAACTGAAAATATCATTTCCAGAAGTTGTC	1321 TATCGTGTTATTGGATTAAGTGGTGATACCCCAACTGAAAATATCATTTCCAGAAGTTGTC 1380

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1 gcgcgccggcctgagagccc.....aaaatgattgttttactctg 3365
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2: gb_htg:*
3: gb_in:*
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1270	1258	2050	1204	1284	1392	2468	1443	2028	1776	1776	3078	3771	3771	2540	3373	3372	3380	3380	% Query Match Length
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AX098236	AX098232	BC004031	BC007966	AX300838	AR379503	BC025508	AX300841	CQ729104	AK056293	AX714144	AY075132	AF374384	CQ777379	BC078180	AY017378	AX300832	AF095844	CQ776470	ID
AX098236 Sequence	AX098232 Sequence	BC004031 Mus muscu	BC007966 Homo sapi	AX300838 Sequence	AR379503 Sequence	BC025508 Mus muscu	AX300841 Sequence	CQ729104 Sequence	AK056293 Homo sapi	AX714144 Sequence	AY075132 Mus muscu	AF374384 Mus muscu	CQ777379 Sequence	BC078180 Homo sapi	AY017378 Homo sapi	AX300832 Sequence	AF095844 Homo sapi	CQ776470 Sequence	Description

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8.5	8.5	8 .5	8.5	9.0	9.8	9.8	10.0	10.6	10.9	11.0	11.2	11.4	13.1	13.5	13.5	13.5	13.5	15.1	15.1	15.1	15.1	18.5	19.7	19.7	
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AC111919 Rattus no			150897 Sequence /	AC007750 Homo sap1								BC019605 Mus muscu	CQ729107 Sequence			CQ152744 Sequence		9		CQ139716 Sequence					

## ALIGNMENTS

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HUCVONMRENEPENAHILIEDMOSTHEKKMKTKRINIAKHYKNPSLIFELCKNCSVLA
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VHKGLDLPCLKIRNVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED"

    (bases 1 to 3380)
    Kang, D.C., Gopalkrishnan, R.V., Wu, Q., Jankowsky, E., Pyle, A.M. and
Fisher, P.B.

                                                                                   Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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2 (bases 1 to 3380)
2 (bases 1 to 3380)
Kang, D.-C. and Fisher, P.B.
Direct Submission
Submitted (30-SEP-1998) Urology, Columbia University, P&S, '
Submitted (30-SEP-1998) Urology, Columbia University, P&S, '
MI68th, New York, NY 10032, USA
Location/Qualifiers
                                                                                                                                            mda-5: An interferon-inducible putative RNA helicase with double-stranded RNA-dependent ATPase activity and melanoma growth-suppressive properties
Proc. Natl. Acad. Sci. U.S.A. 99 (2), 637-642 (2002)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HO-1"
/tissue_type="melanoma"
                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                            AF095844.1 GI:11344593
                                                        Homo sapiens (human)
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    complete cds.
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Best Local Similarity 100.
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GCTGAAGTAGGAGTCAAAGCCCACCATCTGATTGGAGCTGGACACAGCAGTGAGTTCAAA
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AF095844 3380 bp mRNA linear PRI 23-JAN-2002 Homo sapiens melanoma differentiation associated protein-5 (MDA5)

RESULT 2 AF095844 LOCUS DEFINITION

6 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
191 TATTICCACAGACAGATTICCCCTATICTCATCTCCTCCTCCTCCACCACACAGACAGAATTICCCCTATICTCATCTCCTCCTCCTCCACCACCACAGACAGAATTICCCCTATICTCATCTCTCTCCTCCTCCACCACCACACAGACAGAATTICCCCTATICTCATCTCTCTCCTCCTCCCTCCTCACCAGAGATTICCCCTCTCCTCT

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155. ..3232

// Code = "unnamed protein product"
// Codon starte.
// Codon
      PAT 30-NOV-2001
                                                                                                                                                                                           Bahr,G., Cocude,C. and Capron,A.
Rhile polypeptides and its fragments and polynucleotides encoding said polypeptides and therapeutic uses patent: WO 0185955-A 15-NOV-2001, Istac (FR); INSTITUT PASTEUR DE LILLE (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Capron, A. and Bahr, G.M.
Direct Submission
Submitted (09-JAN-2001) Laboratoire d'Immunologie Moleculaire de Submission
1'Infection et de l'Inflammation, Institut Pasteur de Lille, 1 and Professeur Calmette BP 245, Lille 59019, France
Location/Qualifiers
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  J. Gen. Virol. 84 (12), 3215-3225 (2003)
2 (Dases 1 to 3373)
Cocude,C., Kolesnitchenko,V., Billaut-Mulot,O., Truong,M.-J.,
Capron,A. and Bahr,G.M.
Identification of a new RNA helicase (RH116) regulated by the immunomodulator Murabutide
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches 7;
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/mol_type="mRNA"
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3 (bases 1 to 3373)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 3373)
Cocude, C., Truong, M.-J., Billaut-Mulot, O., Delsart, V.,
Darcissac, E., Capron, A., Mouton, Y. and Bahr, G.M.
A novel cellular RNA helicase, RH116, differentially regulates cell
growth, programmed cell death and human immunodeficiency virus type
I replication
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Homo sapiens RNA helicase-DEAD box protein RH116 mRNA, complete
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Strausberg, N. L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares M.B., Bonaldon, M.F., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunartne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, E., Ketteman, M., Maddan, A., Rodrigues, S., Sanchez, A., Whiting, M., Maddan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,	Dickeon,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schlain,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences human and mouse cDNA sequences 2 (Dasses I to 2540) 2 (Dasses I to 2540) Strausberg,R. Direct Submission Submitted (19-JUL-2004) National Institutes of Health, Mammalian	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help deak Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Dy: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;	Contact: nisc mgc@nlgri.nh.gov/ Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Blakesley,R.W., Bouffard,G.G., Groupta,J., Haghighi,P., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,SL., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Madulo,Q.L., Masiello,C., Maskeri,B., Mastrians,B.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Tuchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,LH. and Green,E.D.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 174 Row: p. Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27886567. Location/Qualifiers 12540 //organism="Homo sapiens" //mol_type="mRNA" //mol_type="mRNA"	/tissue_trans
REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	REWARK COMMENT		FEATURES	
	270 270 276 276 283 283	OY 2895 CTGCAGTCTGCTAGCGGAACATATCCATGTAATTGAGAAAATGCCATCACGT 2954	Qy         3075 AACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCAAAATAAGGAATTTTGTAGT 3134           Db         3061 AACAATGATGGTGCACAAAGGGCTTAGGTTTGCCTTGTCTCAAAATAAGGAATTTTGTAGT 3120           Qy         3135 GGTTTTCAAAAATAATTCAACAAGAAACAATACAAAAAGTGGGTAGAATTACCTATCAC 3194           Db         3121 GGTTTTCAAAAATAATTCAACAAGAAAAAGTGGGGTAGAATTACCTATCAC 3180           Qy         3195 ATTTCCCAAATAATTCAACAAAAGAAACAATTAGAAAAAGTGGGGTAGAATTACCTATCAC 3180	Db   3181   ATTTCCCAATCTTGACTATTCAGAATGCTGTTATTTAGTGATGAGGATTAGCACTTGAT   3240	RESULT 5 BC078180 LOCUS BC078180 LOCUS DEFINITION Homo sapiens interferon induced with helicase C domain 1, mRNA ACCESSION FC0NA clone IMAGE:6502757), partial cds. ACCESSION BC078180. GI:50415794 KEYWORDS SOURCE Homo sapiens CRGANISM Homo sapiens Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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cal Similarity 99.8%;
2479; Conservative 0
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Best Local Similarity 80.7%; Pred. No. 0;   Matches 2609;   Conservative 0;   Mismatches 616;   Indels 7;   Gaps 3;   Qy   121   CAGCACCATCTGCTTGGGAGAACCTCTCCC-TTCTCTGAGAAAGAAGATGTCGAATGG 179	QY 180 GIATTCCAGAGATTTCCGCTATCTCGTGCTTCAGGGCCAGGGTGAAAT 239	OY 240 GTACATCCAGGTGGAGCTGTGCTGACTTACTGCTGCAGAGGTGAAGGA 299	OY 300 GCAGATTCAGAGGACAGTCGCCACCTCCGGGAACATGCAGGCACTTGAACTGCTGCTGAG 359	Qy         360 CACCTTGGAGAGGGGCTCGGGAACTTGGGAATTCGTGGAGGCCCTCCG         419	QY 420 GAGAACCGGGAGCCCTCTGGCCGCCTACATGAACCCTGAGGACTTGCCCTC 479	OY 480 TCCATCGTTTGAGAACGCTCATGAATATCTCCAACTGCTGAACCTCTTCAGCCCAC 539	OY 540 TCTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAGGAACTGTT 599	Qy 600 GACAATTGAAGACGGATTGCTGCTGCAGAAAACAATGGAAATGAATG	QY 660 AAGAGGCTACTAAAAGGATTGTGCAGAAAGAAAACTGGTTCTGGATTTCTGAATGT 719	QY 720 TCTTCGTCAAACAAGAAACAATGAACTTGTCCAAGAGTTAACAGGCTCTGATTGGTCAGA 779 	Oy 780 AAGCAATGAGAATTATATCACAAGTTGATGGTCCTCAAGTGGAAGAGCAACT 839	OY 900 ATCAGAATCATTTGCAGATTCTTCTQTAGTTTCAGAATCAGACACAAGTTTGGCAGA 959	QY 960 AGGAAGTGTCAGCTGCTTAGATGAAAGTCTTGGACATAACAGCAACATGGGCAGTGATTC 1019 	QY         1020 AGGCACCATGGGAAGTGATTCAGATGAAGAQAATGTGGCAGCAAGAGCATCCCCGGA 1076	OY 1077 GCCAGAACTCCAGGTCAGGCCTTACCAAATGGAAGTTGCCCAGCCTTGGAAGGGAA 1136	Qy 1137 GAATATCATCATCTGCCTCCTACAGGGAGTGGAAAAACCAGAGTGGCTGTTTACATTGC 1196
Db 1856 ACCAGAGAAGATCCATTTAAAGAGAAACTTCTAGAAATAATGACAAGGATTCAAACTTAT 1915  Qy 1861 TGTCAAATGACCAATGTCAGATTTTGGAACTCAACCCTATGAACAAGGCCATTCAA 1920  Db 1916 TGTCAAATGACTCAATGTCAGATTTTGGAACTCAACCCTATGAACAATGGGCCATTCAA 1920  Db 1916 TGTCAAATGAGTCCAATGTCAGATTTTGGAACTCAACCCTATGAACAATGGGCCATTCAA 1975	Qy 1921 ATGGAAAAAAGCTGCAAAAAAGGAAATCGCAAAGAACGTGTTTGTGCAGAACATTTG 1980  DD 1976 ATGGAAAAAAAGCTGCAAAAGAAAGGAAATCGCAAAGAACGTGTTTGTGCAGAACATTTG 2035	OY 1981 AGGAAGTACAATGAGGCCCTACAAATTAATGACACAATTCGAATGATAGATGCGTATACT 2040 1981	Oy 2041 CATCTTGAAACTTTCTATAATGAAGAAGATAAGAAGTTTGCAGTCATAGAAGATGAT 2100  Db 2096 CATCTTGAAACTTTCTATAATGAAGAAAAATAAAGAAGTTTGCAGTCATAGAAGATGAT 2155	Qy 2101 AGTGATGAGGGTGGTGATGATGAGTATTGTGATGGAGGATGAGGATGAT	OY 2161 AAACCTITGAAACTGGATGAAACAGATAGATTCTCATGACTTTATTTTTGAAAACAAT 2220 	OY 2221 AAAATGTTGAAAAGGCTGGAAAACCCAGAATATGAAAATGAAAAAGCTGACCAAATTA 2280 	Qy 2281 AGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCACCACGAGGAATAATCTTT 2340 Db 2336 AGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCACCACGAGGAATAATCTTT 2395	OY 2341 ACAAAAACACGACAGAGTGCATATGCGCTTTCCCAGTGGATTACTGAAAATGAAAATTT 2400 	Qy 2401 GCTGAAGTAGGAGTCAAAGCCCACCATCTGATTGGAGCTGGACACAGCAGTGAGTTCAAA 2460 	Oy 2461 CCCATGACACAGAATGAAAAAA 2484 Db 2516 CCCATGACACAAAAAAAAA 2539	RESULT 6 CQ7773 CQ777379 LOCUS DEFINITION Sequence 1065 from Patent EP1394274. ACCESSION CQ777379 RESION CQ777379 KENDON CQ777379.1 GI:45380363	SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;	REFERENCE 1 AUTHORS Obtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K. TITLE Methods of testing for bronchial asthma or chronic obstructive	JOURNAL Patent: EP 1394274-A 1065 03-MAR-2004, Genox Research, Inc. (JP) FEATURES Location/Qualifiers	or/ om/	y Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="melanoma differentiation associated gene 5-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 CIGITICIGCAGAGACACCITICAGAATCICATCITATICITICAGGCCCAGGCTGAAAT 305
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (1988) 1 to 371)
Kang, D.-C. and Fisher, P.B.
Kang, D.-C. and Fisher, P.B.
Murine homolog of melanoma differentiaion associated gene-5 - a Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
235. 3312
/note=.38NA-dependent ATPase; predicted molecular weight:
115954:50 Dar
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//note="DEXH helicase signature; unclassified site"
3755. .3760
                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3771)
Kang, D.-C. and Fisher, P.B.
Direct Submission
Submitted (26-APR-2001) Urology, Columbia University, P & 1
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               West 168th, New York, NY 10032, USA
Location/Qualifiers
1. .3771
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1228. .1245
/note="ATP binding motif"
                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
                                                                                                                    AF374384.1 GI:20385627
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Best Local Similarity 80.7
Matches 2609; Conservative
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                                                           DEFINITION
                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
RESULT 7
AF374384
LOCUS
                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                 ACCESSION
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1317 ATGGTH CENTRATEGRATHANGING CHARGE CONTROLL AND ATTGGTH AND	2277 ATTAGAAATACCATAATGGAGGAATATACTAGGACTGAGGAATCAGGAAGGA

708

540

768 909 828 99

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661 AÁTGÁGTGTCTTCTGCTGCTGTCGATGÁGTCTAGAGACAGAGACAGAGGCCTGGAACGTA 720
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                 CTTCAGCCCACTCTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAG
                                         crecadeceactricadadericadaritaacaaretricadeacaeridericada
                                                                    GAGGAACTGTTGACAATTGAAGACAGAAACCGGATTGCTGCTGCAGAAACAATGGAAAT
                                                                                   TITCTGAATGITCTTCGTCAAACAGGAAACAATGAACTTGTCCCAAGAGTTAACAGGCTCT
                                                                                                                                                                                               TICCTGGATGTTCTGCGCCAAACTGGAAATGATGCACTATTCCAAGAACTAACAGGTGGA
                                                                                                                                                                                                                              GATTGCTCAGAAAGCAATGCAGAGTTGAGAATTTATCACAAGTTGATGGTCCTCAAGTG
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TINRVOMRYEBEYAHKILEČVVOSILEKKMKVYKSIAŘKOVNDPELITLICKNOSMLV
CSGBNIHVIEROHHVMTPERGLYIVRENKALOKKRADYONNGEIICKGQAMGTMM
VHKGLDLPCLKIRNFVVNFKNNSPKKQYKKWVELPIRPPDLDYSEYCLYSDED
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  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 3078)
Kovacsovics,M., Martinon,F., Micheau,O., Bodmer,J.L., Hofmann,K.
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                                                               Overexpression of Helicard, a CARD-Containing Helicase Cleaved during Apoptosis, Accelerates DNA Degradation Curr. Biol. 12 (10), 838-843 (2002) 22009979
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Kovacsovics, M., Hofmann, K. and Tschopp, J.

Birect Submission
Submitted (24-JAN-2002) Biochemistry, University of des Boveresses 155, Epalinges, VD 1066, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                                                two CARD domains'
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Pred. No. 0;
0; Mismatches 571; Indels
                                                                                                                                                                                                             1. .3078
/organism="Mus musculus"
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/mol_Lype="mRNA"
1. .3078
/note="helicase; contains twoodon_start="lelicase"
/product="HELICARD"
/protein_id="AAL77205.1"
/db_xref="il:18698981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
81.3%;
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04; Conservative
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Best Local Si
Matches 2504,
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                                                                                        JOURNAL
MEDLINE
PUBMED
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TITLE
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                           REFERENCE
                                      AUTHORS
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1592 ACAAACCAGTGATTCCCCTTCCTCAGATACTGGGACTAACAGCTTCACCTGGTGTTGGAG 1651
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Sequence 828 from Patent EP1293569.
AX714144
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/organism="Homo sapiens"
/mol_type="unassigned DNi
/db_xref="taxon:9606"
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TTGTATAGTGATGAAGATTAG 3078
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Homo sapiens
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  2518
                                                                                                                                                                                                                                                                                                                         RESULT 9
AX714144
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
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Pred. No. 0;
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 52.5%;
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TCAAGGAACTTTACATTGTAAGAGAAAACAAAGCACTGCAAAAGAAGTGTGCCGACTATC
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                                              ATTACAAGAATAACCCATCACTAATAACTTTCCTTTGCAAAAACTGCGGTGTGCTGCCT
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Eukaryota, metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PE Corporation (NY) (TS)
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Sequence 15038 from Patent WO02068579.
CQ729104.1 GI:42299782
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/organism="Homo sapiens"
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/organism="Homo sapiens" /wol type="unassigned DN		1474 ATTGCAGATGCAACCAGAGAAGATCCATTTAAAGAGAAACTTCTAGAAATAATGACAAGG 1533	qa
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-radmail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web sites http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                            BC025508 20-JUL-2004 Mus musculus interferon induced with helicase C domain 1, mRNA (CDNA clone IMAGE:5252257), complete cds.
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Submitted (106-MB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                             GAAAGATAAGAAGTTTGCAGTCATAGAAGATGATGATGATGAGGGTGGTGATGATGAGTA
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         through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.Series: IRAK Plate: 56 Row: c Column: 12
This clone has the following problem: The cds is short comparthe longest cds in the locus.
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Rhil6 polypeptides and its fragments and polynucleotides encoding said polypeptides and therapeutic uses
Patent: WO 0185955-A 7 15-NOV-2001;
Istac (FR); INSTITUT PASTERR DE LILLE (FR)
Location/Qualifiers
                                                                                                                                   Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SUMMARIES	AAD17203	ADJ74904	ADN04879	ADQ22237	ABA04908	ADC3 0823	AAD11170	ADJ75813	AAS40960	ADA53260	AA159285	ABA04916	AA161071	ADC32572	ADI30722	ABA04913	AAS41517	AAS01149	AAS01151	AAS91688	AAS01150
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223 577.2 255 653 267.2 268 577.2 27.2 27.2 27.2 27.2 27.2 27.2 27.2	TLT 1 .7203 AAD17203 stand AAD17203; 29-NOV-2001 ( Human melanoma	Human, melan RNA helicase neuroblastom concrast; color central nerv. Homo sapiens Key CDS misc_feature misc_feature polyA_signal WO200164707., 07-SEP-2001; 29-FEB-2000; (UYCO) UNIV Fisher PB, )
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Nucleic acid sequences encoding a Melanoma Differentiation Associated Gene useful for cancer cell growth suppression, apoptosis and anti-viral activity.
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WPI; 2001-565494/63.
P-PSDB; AAE10155.
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The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IFN) inducible gene with structural influrations to RNA helicases and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the antileukaemic compound mezerain (MEZ). Mda-5 is useful for identifying compounds that may induce its expression. Mda-5 is useful for treating compounds that may induce its expression. Mda-5 is useful for treating compounds that may induce its expression. Mda-5 is useful for treating cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer of the central nervous system and especially where the cancer is a cancer of the central nervous system and apoptosis. The Mda-5 promoter exhibits melanocyte tissue specificity and minimises systemic toxicity. The present sequence is human Mda-5 CDNA

Sequence 3365 BP; 1138 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

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3365; No. 0;	Mismatches TGGACAACCTCG	AACCTCG	GCGGCAC	GCGGCAC	TCCCTTC	TCCCTTC	CTCATC	CTCATC	TACCTG	TACCTG	GGGAAC	GGGAAC	regries.	recried	CTACATG	CTACATG	ATATCTC	ATATCTC	CGTCTTG	CGTCTTG	TGCTGCA	
	Conservative 0; Mismatches 0; Indels 0; Gaps CGCCGGCCTGAGACACCTCGTCATTGTCAGGCACAGAGCGGTAGAC		CCTGCTTCTCTAAGTGGGCAGCGGACAGCGGCACGCACTTTCACCTGTCCCGCAGACAA	GCGGACA	CAGCACCATCTGCTTGGGAGAACCCTCTCCCTTCTCTGAGAAAGAA	cageaccatctgcttgggagaaccctctcccttctcagaaagaa	TATTCCACAGACGAGAATTTCCGCTATCTCATCTCGTGCTTCAGGGCCAGGGTGAAAATG		TACATCCAGGTGGAGCCTGTGCTGGACTACCTGACCTTTTCTGCCTGC	TACATCCAGGTGGAGCCTGTGGTTGGCTACCTGACCTTTCTGCCTGC	CAGATTCAGAGGACAGTCGCCACCTCCGGGAACATGCAGGCAG		ACCTTGGAGAAGGGAGTCTGGCACCTTGGATTGGACTCGGGAATTCGTGGAGGCCCTCCGG	accirgeagaaggaagicigecaccirdeirigeacicgegaairceigeaggccrccge	AGAACCGGCAGCCCTCTGGCCGCCCGCTACATGAACCCTGAGCTCACGACTTGCCCTCT	AGAACCGGCAGCCCTCTGGCCGCCGCTACATGAACCCTGAGCTCACGGACTTGCCCTCT	ATGATGA	ATGATGA	TTAGAGA	TTAGAGA	GGATTGC	
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lery Match	55.		61	61	121	121	181	181	241	241	301	301	361	361	421	421	481	481	541	541	601	
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<u>ک</u> ۾	721 (	CITCGICAAACAGGAAACAAIGAACITGICCAAGAGITAACAGGCICTGAITGCICAGAA 780 
<u>ک</u> و	781	781 AGCAATGCAGAGATTGAGAATTTATCACAAGTTGATGGTCCTCAAGTGGAAGAGCAACTT 840 
a k	841	CTTTCAACCACACTTCAGCCAAATCTGGAGAAGGAGGTCTGGGGCATGGAGAATAACTCA 900
දු .	841	CTTTCAACCACAGTTCAGCCAAATCTGGAGAAGGAGGTCTGGGGCATGGAAATAACLCA 900 maaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
상 음 당	901	TCAGAATCATCTTTTGCAGATTCTTCTGTAGTTTCAGAATCAGACACAGATTTGCAGAA 960
δ	961	GGAAGTGTCAGCTGCTTAGAAGTCTTGGACATAACAGCAACATGGCAGTGATTCA 1020
DP	961	ggadergregeriadargandangertegacaraacagcaacatgggcagtgattca 1020
λo d	1021	GGCACCATGGGAAGTGATTCAGATGAAGAATGTGGCAGCAAGAGGATCCCCGGAGCCA 1080 
a 8	1081	GAACTCCAGCTCAGGCCTTACCAAATGGAAGTTGCCCAGCCAG
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λ	1141	ATCATCATCTCCCTCCCTACAGGGAGTGGAAAAACCAGAGTGGCTGTTTACATTGCCAAG 1200
Op	1141	ATCATCATCTGCCTCCCTACAGGGAGTGGAAAAACCAGAGTGGCTGTTTACATTGCCAAG 1200
λŏ	1201	GATCACTTAGACAAGAAGAAAAAAGCATCTGAGCCTGGAAAAGTTATAGTTCTTGTCAAT 1260
Db	1201	GATCACTTAGACAAGAAGAAAAAGCATCTGAGCCTGGAAAAGTTATAGTTCTTGTCAAT 1260
δ	1261	AAGGTACTGGTAGTTGAACAGCTCTTCGCAAGGAGTTCCAACCATTTTTGAAGAAATGG 1320
qq	1261	AAGGTACTGCTAGTTGAACAGCTCTTCCGCAAGGAGTTCCAACCATTTTTGAAGAATGG 1320
ò	1321	TATCGIGITATIGGATTAAGIGGIGATACCCAACTGAAAATATCATTTCCAGAAGITGTC 1380
qq	1321	TATCGTGTTATTGGATTAAGTGGTGATACCCAACTGAAAATATCATTTCCAGAAGTTGTC 1380
ò	1381	AAGTCCTGTGATATTATCAGTACAGCTCAAATCCTTGAAAACTCCCTCTAAACTTG 1440
qq	1381	AAGTCCTGTGATATTATTATCAGTACAGCTCAAATCCTTGAAAACTCCCTCTTAAACTTG 1440
λ	1441	GAAAATGGAGAAGATGCTGGTGTTCAATTGTCAGACTTTTCCCTCATTATCATTGATGAA 1500
ф	1441	GAAAATGGAGAAGATGCTGGTGTTCAATTGTCAGACTTTTCCCTCATTATCATTGAA 1500
λ̈́o	1501	TGTCATCACCACCAACAAGCAGCAGTGTATAATAACATCATGAGGCATTATTTGATGCAG 1560
дg	1501	TGTCATCACACCAACAAAGAAGCAGTGTATAATAACATCATGAGGCATTATTTGATGCAG. 1550
ζ	1561	AAGTTGAAAAACAATAGACTCAAGAAAGAAACAAACCAGTGATTCCCCTTCCTCAGATA 1620
QQ	1561	AAGTTGAAAAACAATAGACTCAAGAAAGAAAACAAACCAGTGATTCCCCTTCCTCAGATA 1620
δγ	1621	CTGGGACTAACAGCTTCACCTGGTGTTGGAGGGGCCACGAAGCAAGC
Op	1621	CTGGGACTAACAGCTTCACCTGGTGTTGGAGGGGCCACGAAGCAAGC
ζŏ	1681	CACATTTTAAAACTATGTGCCAATCTTGATGCATTTACTATTAAAACTGTTAAAGAAAC 1/4
QΩ	1681	CACATITITAAAACTATGTGCCAATCTTGATGCATTTACTATTAAAACTGTTAAAAAAAA

comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

SEQ ID NO 156; 241pp; English

The present invention describes a method of testing for bronchial asthmma cor circulations obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the capression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (31) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (82) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (22) whose expression levels decrease when respiratory epithelial cells are testing for bronchial asthma or chronic obstructive pulmonary disease; (c) a kit for screening for a candidate compound for a therapeutic agent (2) a kit for screening for a candidate compound for a therapeutic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a natimal model for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, cobstructive pulmonary disease, (a) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, copernession of the gene through an RNAi effect or an antibody recognising compression of the gene through an RNAi effect or an antibody recognising copronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene, and for a bordial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent invention.

C sequence is used in the exemplification of the present invention. for bronchial asthma testing describes a method of

Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

AGAACCGGCAGCCCTCTGGCCGCCCGGTACATGAACCCTGAGGTCACGGACTTGCCCTCT 480 180 240 240 300 360 420 480 120 120 180 9 9 racarccaderdeadecrerecreacracereacerrecerecerecadades ACCTTGGAGAAGGGAGTCTGGCACCTTGGTTGGACTCGGGAATTCGTGGAGGCCCTCCGG cadcatcatcregatagaaccererecerrereagaaagaaagargregaargag CCTGCTTCTCTAAGTGGGCAGCGGACAGCGGCACGCACTTTCACCTGTCCCGCAGACAA TATTCCACAGACGAGAATTTCCGCCTATCTCATCTCGTGCTTCAGGGCCAGGGTGAAAATG GCGCCCCGGCCTGAGAGCCCTGTGGACAACCTCGTCATTGTCAGGCACAGAGCGGTAGAC Gaps ö DB 12; Length 3380; 0; Indels 100.0%; Score 3365; 100.0%; Pred. No. 0; ive 0; Mismatches Query Match Best Local Similarity 100. Matches 3365; Conservative 361 61 61 121 121 181 181 241 241 301 301 361 121 셤 ò g 8 8 ò g ò g ò ઠે 요 ò

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Dp	481	CCATCGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTCCTTCAGCCCCACT 540
δ	541	CTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAGGAGGAGGAGTGTTG 600
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Db	721	CTTCGTCAAACAGGAAACAATGAACTTGTCCAAGAGTTAACAGGCTCTGATTGCTCAGAA /80
ò	781	AGCAATGCAGAGATTGAGAATTTATCACAAGTTGATGGTCCTCAAGTGGAAGAGCAACTT 840
Вр	781	AGCAATGCAGAGATTGAGAATTTATCACAAGTTGATGGTCTCAAAGTGCAAAGAAGAAAAAAAA
δλ	841	CTTTCAACCACAGTTCAGCCAAATCTGGAGAAGGAGGTCTGGGGGATGGAGAATAACTCA 300
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	RESULT 3 ADNO4879 ID ADNO4879 standard; CDNA; 3379 BP. XX AC ADNO4879; XX XX DT 01-JUL-2004 (first entry) XX
1561   MGTTGNAMACATTGACTCAGAAACAAACAACACTGTTCTCCCGTTCTTCGATA   1620   1561   MGTTGAAAACATACACCACTGATTCCCCTTCTTCGATA   1620   1561   MGTTGAAAACATACACTGATTCACTCTCTCTCACAAAACAACACACTGAATCATTCACTTCTCACACTTCACTTGATCACTT	2341 ACAAAACGACAGAGTGCATATGCGCTTTCCCAGTGGATTACTGAAAATTT 2400 2341 ACAAAACACGACAGAGTGCATATGCGCTTTCCCAGTGGATTACTGAAAATTT 2400 2341 ACAAAACACGACAGAGTGCATATGCGCTTTCCCAGTGGATTACTGAAAATTT 2400 2401 GCTGAAGTAGAGTCAAAGCCCACCATCTGATTGGACCTGGAAAATGAAATTT 2400 2401 GCTGAAGTAGAGACACAAACAACACACTGAATTAGAAATTTCGCAGTGAAATTCAAA 2460 2401 GCTGAAGTAGAACAAAAAAAAAAAAAAAAAAATTTCGAACACAGAAAATCAAA 2460 2461 CCCATGACACAGAATGAACAAAAAAAAAAAAAATTTCGCACTGGAAAAATCAAT 2520 2521 CTGCTTATCGCTACCACAGGCAGAAAAAAAAAAATTTCGCACTGGAAAAATCAAT 2580 2521 CTGCTTATCGCTACCACAGGGCAGAAAAGAAGTCTTTAGTAAATTTAAAAAATTAAAAAATATTT 2580 2521 CTGCTTATCGCTACCACAGGGCAGAAAAGAAGTCATTAAAAAATTAAAAAAATTTTT 2580 2521 CTGCTTATGGTCTCCACAGGCAGAAAAAAAAAGAACCAAGAAAATTTAAAAAAAA

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                                                                                                                                                                                                                The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
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The invention relates to a novel method for detecting soft tissue sarcome which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic soil sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. 8  $\times$  9  $\times$  9

Sequence 3668 BP; 1215 A; 730 C; 811 G; 872 T; 0 U; 40 Other;

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                                                                                                                                                                                             Human; RHI16; RNA helicase; cytostatic; virucide; anti-HIV; immunosuppressive; immunostimulatory; antirheumatic; antiarchricatericosclerotic; osteopathic; antidiabetic; hepatrotropic; antinitlammatory; cancer; infection; HIV; hepatitis; genetic disease; autoimmune disease; graft rejection; vaccine; ss.
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           The present sequence is the coding sequence for human RH116. RH116 is a 116kDa protein and has homology to RNA helicases (DEXH box). HH116 and its coding sequence are useful for treating cancer; acute box chronic infections (especially by HV or hepatitis B or C); inherited genetic diseases; (auto)immune diseases (particularly rheumatism, arthritis, arteriosclerosis and diabetes, but many others listed) and to prevent graft rejection. HH116 and its coding sequence are also useful for inducing, or increasing, the immune response to a vaccine
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                                                                                                   GAATTICCGCTATCTCATCTCGTGCTTCAGGGCCAGGGTGAAAATGTACATCCAGGTGGA
                                                                                                                                                                                Score 3338.8; DB 6; Length 3372;
Pred. No. 0;
0; Mismatches 7; Indels 0;
                                                                 Sequence 3372 BP; 1157 A; 637 C; 748 G; 830 T; 0 U; 0 Other;
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Best Local Similarity 99.8%;
Matches 3343; Conservative 0
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New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the
    GAAGTGTGCCGACTATCAAATAAATGGTGAAATCATCTGCAAATGTGGCCAGGCTTGGGG
                               AACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCAAAATAAGGAATTTTGTAGT
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recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of polynucleotides or polypeptide of the invention; and methods of carrying out the methods of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes or invention; methods for the identification of compounds that modulate the cypression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the compounds that modulate the contigue of the invention are contigued in diagnostics, drug screening, forensice, gene mapping, in the useful in diagnostics, drug screening, forensice, gene mapping, in the traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are cide mutations responsible for genetic disorders and other neurodegenerative diseases, ansemia, platelet concerned. The nucleic acids may also be used as hybridisation probes or concerned and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, are also useful in generating antibodies, as molecular weight markers, are also useful in generating antibodies, as molecular weight markers, are also useful in generating antibodies, as molecular weight markers, concerned as food supplements. The present sequence represents a specifically contained human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printer expression as percentages. ftp.wipo.int/pub/published\_pct\_sequences.

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for cancer cell growth suppression, apoptosis and anti-viral Gene useful

Page 134-148; 152pp; English Disclosure;

The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IRW) inducible gene with structural similarities to RNA helicases and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the antileukaemic compound mezerein (MEZ). Mda-5 is useful for identifying compounds that may induce its expression. Mda-5 is useful for treating cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer of the central nervous system and especially where the cancer is a cancer of the central nervous system and appotosis. The Mda-5 promoter exhibits melanocyte tissue specificity and minimises systemic toxicity. The present sequence is designated SEQ ID NO:2 in the sequence listing, but does not correspond to the sequence designated SEQ ID NO:2 in the main referred to in the specification, and has been represented in a protein referred to the testing 

Sequence 3131 BP; 1075 A; 583 C; 699 G; 774 T; 0 U; 0 Other;

7 648 540 768 600 348 408 240 468 528 588 420 480 708 GATTGCTCAGAAAGCAATGCAGAGATTTGAGAATTTATCACAAGTTGATGGTCCTCAAGTG 828 288 120 180 300 GACTTGCCCTCTCCATCGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTC 360 9 CTTCAGCCCACTCTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAG GAGGAACTGTTGACAATTGAAGACAGAAAACCGGATTGCTGCTGCTGCAGAAAACAATGGAAAT TITCIGAATGITCTICGICAAACAGGAAACAATGAACTIGICCAAGAGITAACAGGCICI 1 ArgregaArgggrArrecaeagaegagaArrrecgerarerearcregreerreaggee CIGCTGCTGAGCACCTTGGAGAAGGGAGTCTGGCACCTTGGTTTGGACTCGGGAATTCGTG GAGGCCCTCCGGAGAACCGGCAGCCCTCTGGCCGCCGCCTACATGAACCCTGAGCTCACG GAGGCCCTCCGGAGAACCGGCAGCCCTCTGGCCGCCGCTACATGAACCCTGAGCTCACG GACTTGCCCTCTCCATCGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTC CTTCAGCCCACTCTGGTGGACAAGCTTCTAGTTAGATAGGTCTTGGATAAGTGCATGGAG GAGGAACTGTTGACAATTGAAGACAGAAACCGGATTGCTGCTGCAGAAAACAATGGAAAT ATGTCGAATGGGTATTCCACAGACGAGAATTTCCGCTATCTCATCTCGTGCTTCAGGGCC Gaps ري . Length 3131; 0; Indels 4; DB Score 3104; DB Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 99.8%;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises (a) a group of genes (31) whose expression levels increase when respiratory epithalial cells are stimulated with interleukin-13; or (b) a group of genes (32) respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; gene; therapy; marker gene; ds. disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject. ž pulmonary Izuhara

whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to trreat bronchial asthma or chronic obstructive pulmonary disease; (3) a inducer that induces bronchial asthma in a mouse; (5) a cathma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (5) a cathma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisene nucleic acid corresponding to a portion of the marker gene nucleic acid corresponding to a portion of corpression of the gene through an RNAi effect or an antibody recognising crockin encoded by a marker gene; and (7) a DNA chip for testing for a protein encoded by a marker gene; and (7) a DNA chip for testing for corporation asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory conditional asthma or chronic obstructive pulmonary disease. The present corporation of the present invention. 5555555555555555555555555**%**&

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Sequence 3771 BP; 1183 A; 821 C; 866 G; 901 T; 0 U; 0 Other;

539 605 599 665 629 725 719 785 845 839 479 545 419 245 299 359 425 485 305 aagcaatgcagagattgagaatttatcacaagttgatggtcctcaagtggaagagcaact CACCTTGGAGCAGGGACAATGGCCTCTGGGATGGACGCAGATGTTCGTGGAGGCCCTAGA AAGAGGCTACTAAAAAGGATTGTGCAGAAAGAAAACTGGTTCTCTGCATTTCTGAATGT TCTTCGTCAAACAGGAAACAATGAACTTGTCCAAGAGTTAACAGGCTCTGATTGCTCAGA CACCTTGGAGAAGGGAGTCTGGCACCTTGGTTGGACTTCGTGGAGGCCCTCCG TCCATCGTTTGAGAACGCTCATGATGAATATCTCCCAACTGCTGAACCTCCTTCAGCCCAC TCTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAGGAGGAACTGTT TTTGGTGGACAAACTTCTGATTAACGATGTCTTGGACACTTGCTTCGAGAAGGGACTATT GACAATTGAAGACAGAAACCGGATTGCTGCTGCAGAAAACAATGGAAATGAATCAGGTGT GACAGTCGAAGACAGAAATCGGATTTCTGCTGCAGGAAACAGCGGGAATGAGTCAGGGTGT GAGAACCGGCAGCCCTCTGGCCGCCGCTACATGAACCCTGAGCTCACGGACTTGCCCTC CAGCACCATCTGCTTGGGAGAACCCTCTCCC-TTCTCTGAGAAAGAAAGATGTCGAATGG cedecedecedeceddadaderedreredadadacerededareda GTATTCCACAGAGAATTTCCGCTATCTCATCTCGTGCTTCAGGGCCAGGGTGAAAT 7; Gaps Score 2202.4; DB 12; Length 3771; Pred. No. 0; 0; Mismatches 616; Indels 7; C 65.5%; 80.7%; Query Match Best Local Similarity 80.7 Matches 2609; Conservative 360 486 180 546 540 900 999 726 780 426 420 180 246 240 306 300 366 121 186 8 & 8 5 6 8 6 8 6 8 \$ 8 \$ g ð g ò g ઠે D ઠ

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1685 1325 1316 1385 1376 1436 1496 1196 1256 1076 1145 1205 1025 <u>danachaddadchdadchncachddadathddadcadccaaaaadddachchdaddda</u> TGCAACCAGAGAAGATCCATTTAAAGAGAAACTTCTAGAAATAATGACAAGGATTCAAAC rgacaccagagaaaatccaittaaagagaactictagaaattatggcaagcattagac AAACCTIGAICAACIGAAAAACCAAATACAGGAGCCATGCAAGAAGITIGCCATIGCAGA CTTGGAAAATGGAGAAGATGCTGGTGTTCAATTGTCAGACTTTTCCCTCATTATCATTGA IGAAIGICAICACCACCAACAAGAAGCAGIGIATAAIAAIAACAICAIGAGGCAITAIIIGII rdagrigecarcaccaacaagaagagagacaaraacaacarcargagagaararrigaa AGAACACATITIAAAACTAIGIGCCAATCITGAIGCATITACTATIAAAACIGITAAAGA AAAACATATTTAAAATATATGTGCCCAATCTTGATGCCTTTACCATTAAAACAGTGAAAGA <u>chatradectratectraecrearcectrateceraradactrearcecratatragara</u> TGTCAAGTCCTGTGATATTATCAGTACACTCAAATCCTTGAAAACTCCCTTTAAA CAATAAGGTACTGCTAGTTGAACAGCTCTTCCGCAAGGAGTTCCAACCATTTTGAAGAA ATGGTATCGTCTTATTGGATTAAGTGGTGATACCCAACTGAAAATATCATTTCCAGAAGT AGACAACACAGACTTGGCTAACTCGTCTCACAGAGATGGGCCTGCAGCTAATGAGTGTCT AGGAAGTGTCAGCTGCTTAGAAGTCTTCGACATAACAGCAACATGGGCAGTGATTC AGGCACCATGGGAAGTGATTCAGATGAA--GAGAATGTGGCAGCAAGAGCATCCCCGGA GAATATCATCATCTGCCTCCCTACAGGGAGTGGAAAAACCAGAGTGGCTGTTTACATTGC CAAGGATCACTTAGACAAGAAGAAAAAGCATCTGAGCCTGGAAAAGTTATAGTTCTTGT TCTTTCAACCACAGTTCAGCCAAATCTGGAGAAGGAGGTCTGGGGGCATGGAGAATAACTC **ATCAGAATCATCTTTTGCAGATTCTTCTGTAGTTTCAGAATCAGACACAAGTTTGGCAGA** 1857 1926 1737 1866 1437 1626 1617 1686 1677 1746 1806 1797 1377 1506 1497 1566 1557 1086 1146 1137 1206 1197 1266 1257 1326 1317 1386 1026 1020 1077 840 906 900 996 960

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2997 AAACAAAGCACTGCAAAGAAGTGTGCCGACTATCAAATAAAT	### ### ### ### ### ### ### ### ### ##
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14-ANG-2000; 2000US-022547P.

14-ANG-2000; 2000US-022575PP.

14-ANG-2000; 2000US-022575PP.

14-ANG-2000; 2000US-022575PP.

14-ANG-2000; 2000US-022575PP.

14-ANG-2000; 2000US-022575PP.

15-ANG-2000; 2000US-022575PP.

16-ANG-2000; 2000US-022575PP.

17-ANG-2000; 2000US-022575PP.

18-ANG-2000; 2000US-022575PP.

19-ANG-2000; 2000US-022575PP.

10-SEP-2000; 2000US-022594PP.

10-SEP-2000; 2000US-022944P.

10-SEP-2000; 2000US-022944P.

10-SEP-2000; 2000US-022944P.

10-SEP-2000; 2000US-022944P.

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10-SEP-2000; 2000US-022944P.

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10-SEP-2000; 2000US-023944P.

10-SEP-2000; 2000US-023949P.

10-SEP-2000; 2000US-023949P.

10-SEP-2000; 2000US-023144P.

10-SEP-2000; 2000US-023144P.

10-SEP-2000; 2000US-023144P.

10-SEP-2000; 2000US-023149P.

10-SEP-2000; 200US-023149P.

10-SEP-2000; 200US-023149P.

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2000US-0246524P.
2000US-0246525P.
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01-DBC-2000; 2000US-0250160P.
01-DBC-2000; 2000US-0250191P.
05-DBC-2000; 2000US-025198P.
05-DBC-2000; 2000US-025198P.
06-DBC-2000; 2000US-025198P.
08-DBC-2000; 2000US-025186P.
08-DBC-2000; 2000US-025186P. 2000US - 0246527F .
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2000US - 0246610 P .
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2000US - 0249217 P .
2000US - 0249217 P .
2000US - 0249218 P .
2000US - 0249217 P .
2000US - 0249218 P . 2000US-0249265P 2000US-0249297P 2000US-0249309P 2000US-0250160P 2000US-0250160P 2001US-0259678P 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 08-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 217-NOV-2000; 217 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50. P-PSDB; AAU23090. Novel polypeptides and polymucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 4; SEQ ID NO 186; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences polypeptides (Example 1) and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the isomerases or ligases of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagonders including hyperproliferative disorders (e.g. cancer), isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), artheries), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. influence); influenced in gene theritity) and infectious disorders (e.g. influenca). The polymoclectides of the invention can also be used in gene therapy. AAS41684 represent convention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the mulpo at ftp.wipo.int/pub/published\_pct\_sequences

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AAATAAATGGTGAAATCGTGCAAATGTGGCCAGGCTTGGGGAACAATGATGGTGCACA 3091
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ACACAATTCGAATGATAGATGCGTATACTCATCTTGAAACTTTCTATAATGAAGAAAAG
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                                                                                                                                                                                                                                             New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                  Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika Otsuka M, Nagahari K, Masuho Y_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCCACGAAGCCAAAGCTGAAGAACACATTTTAAAACTATGTGCCAATCTTGATG
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Pred. No. 0;
0; Mismatches 5; Indels 0;
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                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 828; 205pp; English
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(REAS-) RES ASSOC BIOTECHNOLOGY
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Best Local Similarity 99.7%;
Matches 1769; Conservative
                                                                                                                                 14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                 21-MAR-2002; 2002EP-00006586
                                                                                                                                                                                     Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                        2003-395539/38.
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              coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sic acids and polypeptides, useful for treating disorders such nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral soleroals; SNy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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Goodrich R, Drmanac RT;
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in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral seclerosls, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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immunosuppressive; immunostimulatory; anticheumatic; antiarthric;
antiarteriosclerolic; osteopathic; antidiabetic; hepatrotropic;
antiinflammatory; cancer; infection; HIV; hepatitis; genetic disease;
autoimmune disease; graft rejection; vaccine; ds.
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                                                                                                                                                                             The present invention relates to human RH116 (see AAM47798). RH116 is a 116kDa protein and has homology to RNA helicases (DEXH box). RH116 and its coding sequence are useful for treating cancer; caute or chronic infections (especially by H1V or hepatitis B or C); inherited genetic diseases; (auto)immune diseases (particularly rheumatism, arthritis, arteriosclerosis, osteoporosis and diabetes, but many others listed) and to prevent graft rejection. RH16 and its coding sequence are also useful for inducing, or increasing, the immune response to a vaccine. The present sequence was used in an example from the present invention
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                                                                                            New polypeptide, useful for treating and diagnosing cancer or inflammation, and drug screening, comprises a human polynucleotide homologous to RNA helicase.
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches
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INST PASTEUR LILLE.
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                                          Cocude C,
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-UJN-2000; 2000US-00598042.
19-UJL-2000; 2000US-005312.
14-SEP-2000; 2000US-005313.
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                                               AGCTCAAATCCTTGAAAACTCCCTCTTAAACTTGGAAAATGGAGAAGATGCTGGTGTTCA
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                                     AGCTCAAATCCTTGAAAACTCCCTCTTAAACTTGGAAAATGGAGAAGATGCTGGTGTTCA
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                                                                                                                                                                                                                             immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokineiic activity, haemostatic and thrombolytic activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leuksemias and C.N.S disorders. Note: The sequence data for this patent did not form
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                         The invention relates to human nucleic acids (AAIS7798-AAI61369) and the
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                                                                                                                         Claim 1; SEQ ID NO 5060; 10078pp; English
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                                                                                  CATATGCGCTTTCCCAGTGGATTACTGAAATGAAAATTTGCTGAAGTAGGAGTCAAAG 2419
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                                                                                                     CTGAACACCCCTAATATGAAATGAAAAGCTGACCAAATTAAGAAATACCATAATGGAGC
                                             AATATACTAGGACTGAGGAATCAGCACGAGGAATAATCTTTACAAAAACACGACAGAGTG
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New polynuclectide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                 Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporossis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
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                                                                SEQ ID NO:2654.
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Wang D, Ma Y, Asundi
Drmanac RT;
                                                                 Human novel cDNA contig sequence,
       ΒЪ.
       ADC32572 standard; cDNA; 1382
                                                                                                                                                                                                                                     24-SEP-2002; 2002WO-US030474.
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                                               (first entry)
                                                                                                                                                                                                                                                                                                 Zhang J,
Ghosh M, V
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P-PSDB; ADC33339.
                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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Zhou P, Ghosh M,
Haley-Vicente D,
                                                                                                                                                          gene therapy; ss.
                                                                                                                                                                                                WO2003029271-A2.
                                                                                                                                                                              Homo sapiens.
                                               18-DEC-2003
                           ADC32572;
                                                                                                                                                                                                                                                                                                                                                                                                   cancer.
ADC32572
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The invention relates to 971 novel human CDNA sequences (ADC29919-CADC3089) and the polypeptides they encode (ADC30890-ADC31860). The ADC30889) and the polypeptides they encode sequences over 99% identical with convention also relates to nucleic acid sequences over 99% identical with convention of a polypeptide of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting desints a polypeptide of the invention; a method of detecting polymucleotides or polypeptides of the invention; and methods of control invention further discloses methods to peventially, treating or invention further discloses methods of peventially, treating or and/or monoclonal antibodies for carrying out the methods of the invention, methods for the identification of compounds that modulate the and/or monoclonal antibodies for carrying out the methods of the invention or activity of the polymucleotide and/or polypeptide; and 767 expression or activity of the polymucleotide and/or polypeptide; and 767 expression or activity of the polymucleotide and/or polypeptide; and 767 expression or activity of the polymucleotide and/or polypeptide; and 767 expression or activity of the polymptides encoded by the contign (ADC31861-ADC32627) and the polypeptides encoded by the contign (ADC31861-ADC32627) and the polypeptides of the invention are contigned and products dependent on DNA and animo acid sequences. They are data and products dependent on DNA and animo acid sequences. They are also used for treating diseases such as Parkinson's disease or cancer. The nucleic acids may also be used as protein. The polypeptides or primers, and in the recombinant production of a protein. The polypeptides

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Example 2; SEQ ID NO 2654; 1185pp; English.

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ATTCTTTTAAAATACTATCAGTTAAACATTTAATATGATTATGATTAATGTATTCCATAA 1332
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                   GTGTGCTAGCCTGTTCTGGGGAAGATATCCATGTAATTGAGAAAATGCATCACGTCAATA
                                                                                   TGACCCCAGAATTCAAGGAACTTTACATTGTAAGAGAAAACAAAACACTGCAAAAGGT
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    GTGTGCTAGCCTGTTCTGGGGAAGATATCCATGTAATTGAGAAAATGCATCACGTCAATA
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                                                                 TGACCCCAGAATTCAAGGAACTTTACATTGTAAGAGAAAACAAAGCACTGCAAAAGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a composition comprising a plurality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTACAGAACTGACATAAGAATCAATAAAATGATTGTTTTACTCTG 3365
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             and as food supplements. The present sequence represents a human contig
sequence used in an example of the invention. Note: The sequence data for
this patent did not form part of the printed specification, but was
obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
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also useful in generating antibodies, as molecular weight markers, as food supplements. The present sequence represents a human conti
                                                                                                                                                                                                                         CAAATTAATGACACAATTCGAATGATAGATGGTGCGTATACTCCATCTTGAAACTTTCTATAAT
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                                                                                                          Sequence 1382 BP; 513 A; 217 C; 285 G; 367 T; 0 U; 0 Other;
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                                                                                                                                        Score 1316.6;
Pred. No. 0;
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99.1%;
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Matches 1355; Conservative
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Cc for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or constraints the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected to hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes orterlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comprising a microarray and a plurality of polymicleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polymicleotides. The microarray for monitoring confentifying agents for the treatment of the diseases, asthma, confentifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence capresents a human cDNA of the invention. Note: The sequence data for this patent did not form part of from INDAD a sendara usure one will be electronic format directly form inspense. USPTO at segdata.uspto.gov/sequence.html \$

Sequence 1392 BP; 497 A; 215 C; 264 G; 351 T; 0 U; 65 Other;

2515 2455 TCAATCTGCTTATCGCTACCACAGAGGCGGAAGGAGGTCTGGATATTAAAGAATGTAACA 2575 2395 2275 2335 2215 2095 300 360 420 480 900 TAAAGAAACCTTTGAAACTGGATGAAACAGATAGATTTCTCATGACTTTATTTTTGAAA TCTTTACAAAAACACGACAGAGTGCATATGCGCTTTCCCCAGTGGATTACTGAAAATGAAA AATTTGCTGAAGTAGGAGTCAAAGCCCACCATCTGATTGGAGCTGGACACAGCAGTGAGT TCAAACCCATGACACAGAATGAACAAAAAGAAGTCATTAGTAAATTTCGCACTGGAAAAA ACAATAAAATGTTGAAAAGGCTGGCTGAAAACCCCAGAATATGAAAATGAAAAGCTGACCA AATTAAGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCAGCACGAGGAATAA ATACTCATCTTGAAACTTTCTATAATGAAGAAAAGATAAGAAGTTTGCAGTCATAGAAG 1976 ATTTGAGGAAGTACAATGAGGCCCTACAAATTAATGACACAATTCGAATGATAGATGCGT 5; Gaps DB 11; Length 1392; Score 1278.8; DB 11; Lengt. Pred. No. 1.2e-306; 0; Mismatches 77; Indels 38.0%; Best Local Similarity 94.1%; Matches 1311; Conservative 0 2516 2156 2216 241 2276 301 2336 2396 2456 361 421 481 2036 М 121 g 임 상 임 ò 중 음 8 8 셤 ò 셤 ò 셤 ò 임 ⋧ ð

3175 AIGAGGAITAGCACTTGATGAAGATTCTTTTAAAATACTATCAGTTAAACATTTAATAT 3295 3115 2935 2995 1020 3055 2815 2875 1080 2755 TAACTITICCTITICCAAAAACTGCAGTGTGCTAGCCTGTTCTGGGGAAGATATCCATGTAA 960 840 900 1141 AAATAAGGAATTTTGTAGTGTTTTCAAAAATAATTCAACAAGAAACAATACAAAAAGT 3296 GATTATGATTAATGTATTCATTATGCTACAGAACTGACATAAGAATGA TTGAGAAAATGCATCACGTCAATATGACCCCCAGAATTCAAGGAACTTTACATTGTAAGAG azakcazakcieczakakakakarerecekerrarcakarakakarekakarek AATGTGGCCAGGCTTGGGGAACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCA <u>AAATAAGGAATTTTGTAGTGGTTTTCAAAAATAATTCAACAAAGAAACAATACAAAAAGT</u> TTGAGAAAATGCATCACGTCAATATGACCCCAGAATTCAAGGAACTTTACATTGTAAGAG TAACTITICCATAAAAACTIGCAGTGTGCTAGCCTGTTCTGGGGAAGATATCCATGTAA 2816 AAAAGAAAATGAAAACCAAGGAAATATTGCCAAGCATTACAAGAATAACCCATCACTAA ccadadcrdardadadacchaccractidaridcrcacadidaricaddagriaricaad 2696 ATGAGACAGTTAATGATTTCCGAGAGAAGATGATGTATAAAGCTATACATTGTGTTCAAA CCAGAGCTGATGAGAGCACCTACGTCCTGGTTCACAGTGGTTCAGGAGTTATCGAAC 3353 2996 1021 3056 1081 3116 3176 3236 2936 961 2876 2576 2636 661 2756 901 g à 8 ò g ò g g ð g õ g ò ò g g ò ò ò 원 ò 셤 ò 용 à

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STRANDEDNESS: single
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Query Match
 Sequence 403, App
Sequence 4970, Ap
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Sequence 7, Appli
                                                                                  January 27, 2005, 10:52:16; Search time 294 Seconds (without alignments) 8135.390 Million cell updates/sec
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(/ggn2 6/ptodata1/ina/5A_COMB.seq:*

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(/ggn2 6/ptodata1/ina/6A_COMB.seq:*

(/ggn2 6/ptodata1/ina/6B_COMB.seq:*

(/ggn2 6/ptodata1/ina/6B_COMB.seq:*

(/ggn2 6/ptodata1/ina/PCTUS_COMB.seq:*

(/ggn2 6/ptodata1/ina/backfiles1.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-2844
US-09-806-708B-22
US-08-446-855A-1
US-09-150-741-1
US-09-150-741-1
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US-09-221-268D-12
US-08-143-56
US-09-221-268D-11
US-09-221-268D-11
US-09-853-768-10
US-09-853-768-10
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US-09-853-768-10
US-09-834-46
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Maximum Match 100%
Listing first 45 summaries
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28 47.8 1.4 2319 3 US-0-558-489-90 Sequence 90. Appl 29 47.8 1.4 2319 3 US-0-558-489-90 Sequence 91. Appl 20 47.8 1.4 2319 3 US-0-558-478-90 Sequence 91. Appl 20 47.2 1.4 2359 1 US-0-578-302-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-578-301-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 2295 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-577-411-3 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 4080 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1986-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1886-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1886-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1886-1 Sequence 91. Appl 20 47.2 1.4 40.0 1 US-0-525-1886-1 Sequence
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AATGTGGCCAGGCTTGGGGAACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCA 3115
                                                                                                         3236 ATGAGGATTAGGACTTGATTGAAGATTCTTTAAAATACTATCAGTTAAAGATTTAATAT 3295
                                                                                                                                                                                                                            1319 TGTTATGATTAATGTATTCATTATGCTACAGAACTGACAATNGAGNCTCAATAAAAATGA 1378
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                                                                                      <u>AAATAAGGAATTTTGTAGTGGTTTTTCAAAAATAATTCAACAAAGAAACAATACAAAAAGT</u>
                                                                                                                                                 1081 AAIGIGGCCAGGCTTGGGGAACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Hongping
TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY
TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 43563/JPW/AKC TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550 TELEFAX: (212) 664-0525 TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 301 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTE RELEASE #1.0, VEX
SOFTWARE: PATENTION DATA:
APPLICATION WUMBER: US/08/143,576
FILING DATE: 25-CCT-1933
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION WUMBER: 28,678,700.000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08143576
Patent No. 5643761
                                                                                                                                                                                                                                                                                                                                  TTGTTTTACTCTG 3365
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: New York
COUNTY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                        1 ATTTGAGGAAGTACAATGAGGCCCTACAAATTAATGACACAATTCGAATGATAGATGCGT
                             Gaps
                             5,
                               Indels
                             77;
               Best Local Similarity 94.1%; Pred. No. 0;
Matches 1311; Conservative 0; Mismatches
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1048 GAGAATGTGGCAGCAAGAGCATCCCCGGAGCCAGAACTCCAGCTCAGGCCTTACCAAATG 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wentman, Tom
APPLICANT: Wentman, Tom
APPLICANT: Wentman, Tom
APPLICANT: Drmanac, Reena
TITLE OF INVENTION: NO. 6783969el Nucleic Acide and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILIKO DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
                                                           Sequence 771, Application US/09799451
Patent No. 6783969
                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Shou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Rang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
PLICANT: Wang, Jian-Rui
PLICANT: Wang, Jian-Rui
'LICANT: Wang, Zhiwei
ICANT: Wang, Zhiwei
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; LOCATION: (190)..(2223)
US-09-799-451-771
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ORGANISM: Homo sapiens
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Patent No. 6720408
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
APPLICANT: Joingling
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING MDA-7 AND PHARMACEUTICAL COMPOSIT
FILE REFERENCE: A1994-A-A (070050.1637)
CURRENT APPLICATION NUMBER: US/09/221,268D
CURRENT APPLICATION NUMBER: 08/136,537
PRIOR FILING DATE: 1994-09-30
PRIOR FILING DATE: 1993-10-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE FEASTER FOR Windows Version 4.0
                                                                                   1592 ACAAACCAGTGATTCCCCTTCCTCAGATACTGGGACTAACAGCTTCACCTGGTGTTGGAG 1651
                                                                                                                                                                                                    1652 GGGCCACGAAGCAAGCCAAAGCTGAAGAACACTTTTAAAACTATGTGCCAATCTTGATG 1711
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240 TAGAAATAATGACAAGGATTCAAACTTATTGTCAAATGAGTCCAATGTCAGATTTTGGA 298
                                                                                                                                                                                                                                                                                                                                                     180 CATGCAAGAAGTTTGCCATTGCAGATGCAACCAGAGAAGATCCATTTAAAGAGAAACTTC 239
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Pred. No. 2.4e-67;
0; Mismatches 1; Indels 1
                                1; Indels
99.3%; Pred. No. 2.4e-67; tive 0; Mismatches 1
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Best Local Similarity 99.3°
Matches 297; Conservative
  Best Local Similarity 99.3
Matches 297; Conservative
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ORGANISM: homo sapiens
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                                                                                                                             GGAGGGGCCACGAAGCAAGCCAAAGCTGAAGAACATTTTAAAACTATGTGCCAATCTT 1707
                                                                                                                                                                                 GATGCATTTACTATTAAAACTGTTAAAGAAAACCTTGATCAACTGAAAAACCAAATACAG 1767
                                                                                                                                                   cacacergeargearcaceceagaacrecacececageacrecaceacacacacaa 825
CTCACTGTCTTCTCCCTGATCGTGGTGGATGAGTGCCACCACACGCACAAGGACACCGTC 612
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                                                                          GAAAACAAACCAGTGGTTCCCTTCCTCAGATACTGGGACTAACAGCTTCACCTGGTGTT
                                                 613 TACAACGTCATCATGAGCCAGTACCT-----AGAACTTAAACTCCAGAGG
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GANATAGCCATGGTCCAGGCCCGTGGTCGAGCCAGAGCTGATGAGAGCACCTACGTCCTG
                                                                                                                                                                                                                                                                          GTTGCTCACAGTTCAGGAGTTATCGAACATGAGACAGTTAATGATTTCCGAGAGAAG
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APPLICATION NUMBER: US/08/143,576
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-OCT-1993
CLASGIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 43563/JPW/AKC
TELECHONE: (212) 977-9550
TELEPRAX: (212) 664-0525
TELEFRAX: (212) 664-0525
TELER: 425523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-143-576-6
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1876 ATGTCAGATTTTGGAACTCAACCCTATGAACAATGGGCCATTCAAATGGAAAAAAAGCT 1935
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                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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TITLE OF INVERNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Lardner
STREET: 1800 n. . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                    APFLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 83-9300
TELEFAX: (703) 83-4109
                                                                                              STREE: 1800 Diagonal Road, Suite 500 CTTY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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Matches 19; Conserva
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APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Paul B.
APPLICANT: Jiang, Hongping
TITLE OF INVENTION: NUCLBIC ACID MOLECULES WHICH SPECIFICALLY HYBRIDIZE WITH
TITLE OF INVENTION: NUCLBIC ACID SEQUENCE ENCODING MDA-7 AND PHARMACEUTICAL COMPOSIT
TITLE REFERENCE: 134534-A-A (070050.1637)
CURRENT PAPLICATION NUMBER: 08/012.23
PRIOR APPLICATION NUMBER: 08/1145,537
PRIOR APPLICATION NUMBER: 08/1143,576
PRIOR APPLICATION NUMBER: 08/143,576
PRIOR FILING DATE: 1993-10-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3067 GCTTGGGGAACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCAAAATAAGGAAT 3126
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                                                                                                                                                                                                     Length 193;
                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                   Score 124.6; DB 1
Pred. No. 6.2e-24;
0; Mismatches 4
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; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:
                                                                                                                                                                                               3.7%;
                         LENGTH: 193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                               Query Match
Best Local Similarity 96.5
Matches 138; Conservative
         SEQUENCE CHARACTERISTICS:
                                                                         MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENOTH
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Best Local Similarity
Matches 138; Conserv
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Query Match
Best Local Similarity 60.8%;
Matches 101; Conservative
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; LOCATION: (183)...(5957)
US-09-853-768-3
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 91
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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US-09-222-575-46/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2612 certrocaccitrécadagaceerectecatracatrodercerégeceses 2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ray, Animesh
APPLICANT: Ray, Animesh
APPLICANT: Golden, Teresa Ann
TITLE OF INVENTION: GENE ENCODING SHORT INTEGUMENTS AND USES THEREOF
FILE REPERENCE: 176/60581
CURRENT APPLICATION NUMBER: US/09/590, 968B
CURRENT PILING DATE: 2000-06-09
PRIOR PILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
SEQ ID NOS: 18
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG-09-853-768-10
Sequence 10, Application US/09853768
Sequence 10, Application US/09853768
Sequence 10, Application US/09853768
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION FILE REFERENCE: RTS-0217
CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 10
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Score 62; DB 4; I
Pred. No. 4.4e-06;
0; Mismatches, 65;
                                                                                                          Sequence 1, Application US/09590968B Patent No. 6737561
GENERAL INFORMATION:
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Similarity 60.8%;
Ol; Conservative (
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ORGANISM: Homo sapiens
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US-09-853-768-10
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NAME/KEY: CDS
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Best Local Simi
Matches 101;
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GENERAL INFORMATION:
APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 210121.470
CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT APPLICATION NUMBER: US/09/222,575
NUMBER OF SEQ ID NOS: 174
SOPTWARE: FastEEQ for Windows Version 3.0
SEQ ID NO 46
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                                                            2537 CAGTGGCAGAAGAAGGTCTGGATATTAAAGAATGTAACATTGTTATCCGTTATGGTCTCG 2596
298 AACAGGAAGAGGTACTTAGGAAATTTCGAGCACATGAGACCAACCTGCTTATTGCAACAA 357
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Patent No. 6444466
GENERAL INFORMATION:
APPLICANT: Dona T. Watch
APPLICANT: Andrew T. Watch
TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
FILE REFERENCE: RTS-0217
CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
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Pred. No. 8.2e-05;
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Pred. No. 4.9e-06;
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 46
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APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: COMPOSITIONS FOR PILE REPERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339,338A
CURRENT FILLING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
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52.7%; Pred. No. 8.2e-05;
tive 0; Mismatches 144; Indels
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APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
     2854 TACAAGAATAA 2864
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ORGANISM: Homo sapien
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                                                   2555 TGGATATTAAAGAATGTAACATTGTTATCGTTATG-GTCTCGTCACCAATGAAATAGCC 2613
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Patent No. 651827
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchum, Jennifer L.
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-470C3
CURRENT APPLICATION NUMBER: US/09/389,681A
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
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     Gaps
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Matches 164; Conservative
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Matches 164;
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APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT APPLICATION NUMBER: US/09/433,826B
NUMBER OF SEQ ID NOS: 1999-11-03
NUMBER OF SEQ ID NOS: Windows Version 3.0
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1.6%; Score 54.6; DB 4; Length 37
Best Local Similarity 52.7%; Pred. No. 8.2e-05;
Matches 164; Conservative 0; Mismatches 144; Indels
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52.7%; Pred. No. 8.2e-...
0; Mismatches 144;
; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 46; LENGTH: 371
TYPE: DNA; TYPE: DNA; ORGANISM: Homo sapien
US-09-339-338-46
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Sequence 46, Application US/09433826B

Patent No. 6579973

GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
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Best Local Similarity 52.74
Matches 164; Conservative
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ORGANISM: Homo sapien
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Qy 2734 AAAGCTATACATTGTGTCAAAATATGAACCAGAGGAGTATGCTCATAAGATTTTGGAA 2793

Db 186 GACTTTATTTTACGCCTTCAGACATGGACGAGCAGTATTTTAGGGAAAAATTCTGCAT 127

Qy 2794 TTACAGATGCAAAGATAATGGAAAAATGAAAAATGAAAAAATTCTGCAT 127

Db 126 ATACAGAACTCATGAAAAATTCATCAGAGAAAAAAAACCAAAAACCTGTACCTGAT 67

Qy 2854 TACAAGAATAA 2864

Db 66 AAGGAAATAA 56
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Search completed: January 27, 2005, 17:57:24 Job time : 298 secs

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LENGTH: 3365
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| Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/DFOTUS_PUBCOMB.seq:*
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-275-822A-1
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Sequence 25, Appl
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Publication No US200300228531

GENERAL INFORMATION:

APPLICANT: Ficher, Paul B.

APPLICANT: Gopalkrishnan, Rahul V.

TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT

FILE REPRENCE: A34614-A-PCT-USA-A (070050.1921)

CURRENT FILING DATE: 2002-01-22

FRIOR APPLICATION NUMBER: PCT/USO1/06560

PRIOR FILING DATE: 2001-22

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FASEEEQ for Windows Version 4.0
                                                                                          US-10-029-386-24101
US-09-918-995-12953
US-09-907-907A-32
US-10-029-386-10395
US-10-198-846-5938
US-10-417-827-12
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US-10-108-260A-2072
US-10-1012-118-1472
US-10-342-887-1472
US-10-755-889-233
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US-09-864-761-577
US-09-864-761-15269
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US-09-864-761-30598
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US-09-864-761-29164
           US-10-264-049-69
US-10-228-897-25
US-10-055-475-3
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 3365, Conservative
TYPE: DNA
ORGANISM: homo sapiens
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                                                                                   Sequence 1, Application US/10228897
; Sequence 1, Application US/10228897
; Publication Wo. US20030092043A1
; GENERAL INFORMATION:
    APPLICANT: Fisher, Paul B.
    APPLICANT: Kang, Dong-Chul
    APPLICANT: Gopalkrishnan, Rahul V.
    TITLE OF INVENTION: GENE-5 AND PROMOTER AND USES THEREOF
    TITLE OF INVENTION: GENE-5 AND PROMOTER AND USES THEREOF
    TITLE OF INVENTION: GENE-5 AND PROMOTER AND USES THEREOF
    TITLE OF INVENTION: MABBER: US/10/228,897
    CURRENT APPLICATION NUMBER: US/10/228,897
    CURRENT FILING DATE: 2002-08-26
    PRIOR PELICATION NUMBER: 09/515,363
    PRIOR FILING DATE: 2000-02-28
    NUMBER OF SEQ ID NOS: 25
    SOFTWARE: PSEASEQ for Windows Version 4.0
    SEQ ID NO 1.
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ORGANISM: homo sapiens
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AND CONTROLLED CONTROL	AGAATGTTGAAAAGGCTGGCTGAAAACCCAGAATTGAAAATGAAAAGCTGACCAAATTA AGAAATACCATAATGGACTGGTTGAAACCCAGGGAATAATCTTT AGAAATACCATAATGGACAATATACTAGGACTGAGAATCACCACGGGAATAATCTTT ACAAAAACCACACAGAGCAATATACTAGGACTGAATTACTGAAAATGAAAATTCTTT ACAAAAACCACACACACACACATGCATTTCCCAGTGGATTACTGAAAATGAAAATTCTTT ACAAAAACCACACAAATGCACTTTCCCAGTGGATTACTGAAAATGAAAATTTTCTTTACAAATGAAAATTTCAAA CCCATGAACTAGGACACAAAACCCATCTTTTTTCCCAGTGGATTACTGAAAATTCAAA CCCATGAACTAGGAACAAAAACCCATCTTTTTTTTCCACTGGAAAATTTCAAA CCCATGAACTAGGAACACAAAAACCCATCTTTTTTTTTT	2941 AAAATGCATCACGTCAATATGACCCCAGAATTCAAGGAACTTTAAATTGTAAGAAAAAC 3000 3001 AAAGCACTGCAAAAGAAGTGCCGACTATCAAATAATGGTGAAATGT 3060 3001 AAAGCACTGCAAAAGAAGTGTGCCGACTATCAAATAATGGTGAAATGT 3060 3001 AAAGCACTGCAAAAGAAGTGTGCCGACTATCAAAAATGATTGCTTGC
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US-10-198-46-13042
; Sequence 13042, Application US/10198846
; Sequence 13042, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
    APPLICANT: LILIA, James
    APPLICANT: Wardy, Youzhen
; APPLICANT: Steinmann, Kathlen
    APPLICANT: Steinmann, Kathlen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
    TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, FREV
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: RRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT APPLICATION NUMBER: 60/336,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FRALESQ for Windows Version 4.0
; SEQ ID NO 13042
; LENGTH 3928
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 3925, 3926, 3927, 3928
OTHER INFORMATION: n = A,T,C or G
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; Sequence 4, Application US/10055475
; Publication No. US200300228551
; GENERAL INFORMATION:
    APPLICANT: Fisher, Paul B.
    APPLICANT: Gopalkrishnan, Rahul V.
    TITLE OF INVENTION: USE OF WDA-5 AS AN ANTIVIRAL AND TITLE OF INVENTION: USE OF WDA-5 AS AN ANTIVIRAL AND FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
    CURRENT FILING DATE: 2002-01-22
    PRIOR PILING DATE: 2001-02-28
    PRIOR PILING DATE: 2001-02-28
    PRIOR PILING DATE: 2000-02-29
    PRIOR PILING DATE: 2000-02-29
    PRIOR PILING DATE: 2000-02-29
    NUMBER OF SEQ ID NOS: 17
    SOFTWARE: FRAESEQ for Windows Version 4.0
    SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                              DB 14;
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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 3361; Conservative 0
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; ORGANISM: homo sapiens
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Joinnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05892.0193.NPUS01
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 5057
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Sequence 5057, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
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Version 4.0	Query Match 99.2%; Score 3338.8; DB 10; Lengun 33.2; Best Local Similarity 99.8%; Pred. No. 0; 7; Indels 0; Gaps 0; Matches 3343; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	OY 15 GAGCCTGTGGACAACCTCGTCATTGTCAGGCACAGAGCGGTAGACCCTGCTTCTCTAAG 74	OY 75 TGGGCAGGGGACGCACGCACTTTCACCTGTCCGGAGACACACGCCATCTGCT 134	OY 135 TGGGAGAACCTCTCCCTTCTCTGAGAAAGAAGATGTCGAATGGGTATTCCACAGACGA 194	OY 195 GAAITICGGCTAICIGICATCIGGCTGGGCCAGGGTGAAAATGTACATCCAGGTGGA 254	Oy 255 GCCTGTGCTGACTACCTGACCTTCTGCCTGCAGAGGTGAAGGAGCAGATTCAGAGGAC 314	OY 315 AGTCGCCACCTCCGGGAACATGCAGGCAGTTGAACTGCTGAGCACCTTGGAGAAGGG 374	OY 375 AGTCTGGCACCTTGGACTCGGGAATTCGTGGAGGCCCTCCGGAGAACCGGCAGCCC 434	Qy 435 TCTGGCCGCCTACATGAACCCTGAGCTCACGGACTTGCCCTCTCCATCGTTTGAGAA 494	OY 495 CGCTCATGATGATATCTCCAACTGCTGAACCTCCTTCAGCCCACTCTGGTGGACAAGCT 554	555		Db 601 AAACCGGATTGCTGCTGCAGAAAACAATGGAATGAATCAGGTGTAAGAGGCTACTAAA 660	OY 675 AAGGATIGTGCAGAAAGAAAACTGGTTCTCTGCATTTCTGAATGTTCTTCGTCAAACAGG 734	735 AAACAATGAACTTGTCCAAGAGTTAACAGGCTCTGATTGCTCAGAAAGCAATGCAGAGAT	721	Db 781 TGAGAATTATCACAAGTTGATGCTCCTCAAGTGGAAGAGCAACTTCTTTCAACCACAGT 840		
2581 ATCCGTTATGGTCTCGTCACCAATGAAATAGCCATGGTCCAGGCCCGTGGTCGAGCCAGA 2 2641 GCTGATGAGACCTACGTCCTGGTTGCTCACAGTGGTTCAGGAGTTATCGAACATGAG 2 2641 GCTGATGAGAGCACCTACGTCCTGGTTGCTCACAGTGGTTCAGGAGTTATCGAACGTGAG 2 2701 ACAGTTAATGATTCCGAGAGAATGATGATAAAAAGCTATACATTGTGTTCAAAATATG 2 2701 ACAGTTAATGATTTCCGAGAGAAGATGATGATAAAAGCTATACATTGTGTTCAAAATATG 2 2701 ACAGTTAATGATTTCCGAGAGAAGATGATGATAAAAGCTATACATTGTGTTCAAAATATG 2	OY 2761 AAACCAGAGGAGTATGCTCATAAGATTTTGGAATTACAGATGAAAGTATAATGGAAAAG 2820 	QY 2821 AAAATGAAAACCAAGAGAAATATTGCCAAGCATTACAAGAATAACCCATCACTAATAACT 2880	OY 2881 TTCCTTTGCAAAAACTGCAGTGCTGGCTGTTCTGGGGAAGATATCCATGTAATTGAG 2940	OY 2941 AAAATGCATCACGTCAATATGACCCCCAGAATTCAAGGAACTTTACATTGTAAGAGAAAAC 3000	OY 3001 AAAGCACTGCAAAAGAAGTGTGCCGACTATCAAATAAATGGTGAAATGTTGCAAATGT 3060 	OY 3061 GGCCAGGCTTGGGGAACAATGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCAAAATA 3120	Qy 3121 AGGAATTTTGTAGTGGTTTTCAAAAATAATTCAACAAAGAAACAATACAAAAGGTGGGTA 3180	Qy 3181 GAATTACCTATCACATTTCCCAATCTTGACTATTCAGAATGCTGTTTATTTA	Oy 3241 GATTAGCACTTGATTGAAGATTCTTTTAAAATACTATCAGTTAAACATTTAATATGATTA 3300	Qy 3301 TGATTAATGTATTCATTATGCTACAGAACTGACATAAGAATCAATAAAATGGTTGTTTA 3360 bb 3301 TGATTAATGTATTATGCTACAGAACTGACATAAGAATCAATAAAATGATTGTTTA 3360		Db 3361 CTCTG 3365	RESULT 8 US-10-275-822A-1	; Sequence 1, Application US/10275822A ; Publication No. US20040086500A1 ; GENERAL INFORMATION:	; APPLICANT: Banr, Georges ; APPLICANT: Cocude, Cecile ; APPLICANT: Capron, Andre	rapeutic Uses	; CURRENT APPLICATION NUMBER: US/10/275,822A; CURRENT FILING DATE: 2002-11-12; PRIOR APPLICATION NUMBER: PCT/FR01/01441	; PRIOR FILING DATE: 2001-05-11 ; PRIOR PILING DATE: 2000-05-11 ; PRIOR FILING DATE: 2000-05-11	; NUMBER OF SEQ ID NOS: 56

1915   GCCCTACAMATHATGACACAMTGANGATAGANGCANACTACAMATHATGACAMACTTT 2016   2015   CTATAMTGANGAMATHATGACACATAGANGCATCAMACTACAGGGGGG 2114   2011   CTATAMTGANGAMAGATAGANGATTGACATCACACACATCATAGACAGGGGGG 2114   2011   CTATAMTGANGAMAGATAGANGATTGACATCACACACATCATAGANGCATTGACACACACATCATTGACACACACACACACACACA	
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122 CATTTACTATTAAAACTGTTAAAGAAAACCTTGATCAACTGAAAAACCAAATACAGGAGC 181   1772 CATGCAAGAAGTTTGCCATTGCAGATGCAACCAGAGAAGATCCATTTAAAGAGAAACTTC 1831   182 CATGCAAGAAGTTTGCCATTGCAGATGCAGAAGAAGATCCATTTAAAGAGAAACTTC 241   183 TAGAAATAATGACAATGCAGTTTAAACGAACACCAGAAGATCCATTTAAAGAGAAACTTC 241   184 TAGAAATAATGACAATGGCATTCAAACTGAAATGAGACCCAATGTCAGATTTTGGAA 1891   185 CTCAACCCTATGAACAATGGGCCATTCAAATGGAAAAAAGTCCAATGTCAGATTTTGGAA 301   185 CTCAACCCTATGAACAATGGGCCATTCAAATGGAAAAAAAA	422 ACACAATTCGAATGATACATACTCATCTTGAACTTTCTATAATGAAGAAGA 481 2072 ATAAGAAGTTTGCAGTCATAGAAGATGATACTGAGGGGGGGG	2312 CTGAGGAATCACCACGAGGAATAATCTTTACAAAACACGACAGAGTGCATATGCGCTTT 2371 722 CTGAGGAATCACCACGAGGAATAATCTTTACAAAAACACGACAGAGTGCATATGCGCTTT 781 2372 CTGAGGAATCAGCACAGGAATAATCTTTACAAAACACGACAGAGTGCATATGCGCTTT 781 2372 CCCAGTGGATTACTGAAAATGAAAATTTGCTGAAGTCAAAGAGCCCACCATCTGA 2431 782 CCCAGTGGATTACTGAAAATGAAAATTTGCTGAAGTCAAAGAGCCCACCATCTGA 841 2432 TTGGAGCTGGACACAGCAGTGAGTTCAAACCCATGACACAGAATGAAAAAAAA	2552 GTCTGGATATTAAAGAATGTAACATTGTTATCGGTTATGGTCTCACCAATGAAATAG 2611 962 GTCTGGATATTAAAGAATGTAACATTGTTATCGGTTATGGTCTCGTCACCAATGAAATAG 1021 2612 CCATGGTCTAGGCCGGTGGTCGAGCCGAGGCCCTACGTCGCTCGC	AATTACAGATGCAAAGTATATGGAAAAGAAAATGAAAACCAAGAGAAATTTGCCAAGC
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Db 3061 AACAATGATGGTGCACAAAGGATTTGCCTTGTCTCAAATAAGGAATTTTGTAGT 3120  Qy 3135 GGTTTTCAAAATTAATCAACAAGAAACAATACAAAAAGTGGGTAGAATTTCTACAAAATACAAAAATACAAAAAATACAAAAAATACAAAAAA	RESULT 9 US-10-094-749-828 US-10-094-749-828  Sequence 828, Application US/10094749  Publication No. US20030219741A1  GENERAL INFORMATION:  APPLICANT: SOCGAI, TAKAO  APPLICANT: SUGIYANA, TOWOYASU  APPLICANT: SUGIYANA, TOWOYASU  APPLICANT: SHII, SHIZUKO  APPLICANT: SATO, HIROYUKI  APPLICANT: ISHII, SHIZUKO  APPLICANT: ISONO, YUUKO  APPLICANT: ISONO, YUUKO  APPLICANT: HO, YUKA  APPLICANT: NAGAI, KAORU  APPLICANT: NAGAI, KEIICHI  APPLICANT: RIBE, RYOTARO	APPLICANT: TAMECHIRA, ICHIRO APPLICANT: SEKI, NAOHIKO APPLICANT: SEKI, NAOHIKO APPLICANT: YOSHIKAMA, TEUTOMU APPLICANT: OTSUKA, MOTOYUKI APPLICANT: NACAHART, KENI APPLICANT: NACAHART, KENI APPLICANT: MASCHO, YASHIKO ITILE OF INVENTION: NOVEL FULL-LENGTH CDNA FILE REFRENCE: 084335/0.160 CURRENT FILING DATE: 2002-03-12 PRIOR APPLICATION NUMBER: US/350,435 PRIOR FILING DATE: 2002-01-24 PRIOR APPLICATION NUMBER: JP 201-328381 PRIOR FILING DATE: 2002-01-24 NUMBER OF SEQ ID NOS: 3381	o cas a	Oy 1712 CATTTACTATTAAAACTGTTAAAGAAAACCTTGATCAACTGAAAAACCAAATACAGGGC 1771

GAAAGAAAACTGGTTCTCTGCATTCTCGAAACCAATGCAACGGAAACAATGTTC	1287 CCGCAAGGAGTTCCAACCATTTTGAAGAAATGGTATCGTGTTATTGGATTAAGTGGTGA 1346 601 CCGCAAGGAGTTCCAACCATTTTTGAAGAAATGGTATCGTGTTATTTGGATTAAGTGGTGA 660 1347 TACCCAACTGAAAATATCATTTTTGAAGAAATGGTAAATTGGATTAAGTGGTGA 660 1340 TACCCAACTGAAAATATCATTTCCAGAAGTTGTCAAGTGTTTATTATCAGTAC 720 1407 AGCTCAAATCCTTGAAAATTTCCATTGAAAATTGGAAAATGGAGAAGAGTGTTCA 1466 1210 AGCTCAAATCCTTGAAAACTTCCTTAAACTTGGAAAATGGAGAAGAGTGTTCA 1466 1210 AGCTCAAATCCTTGAAAACTTCCTTCATTGAAAATGGAGAAGAGTGCTGGTGTTCA 1466 1210 AGCTCAAATCCTTGAAAACTTGAAGAAATGGAAAAAGAAGAAGAGAGTTCAAGAA 1586 1811 ATTGTCAGACTTTTCCTTCATTATTGATGCAAAATGAAAAACAAAAAAAA
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0y 2852 ATTACAAGAATAACCCATCACTAATAACTTTCCTTTGCAAAACTGCAGTGTGTGCTTGCT	RESULT 10  US-11-25-822A-10  US-11-25-822A-10  US-11-25-822A-10  US-11-25-822A-10  Sequence 10, Application US/10275822A  Publication No. US20040085500A1  CENERAL INFORMATION:  APPLICANT: Bahr, Georges  APPLICANT: Counde, Cecile  APPLICANT: Counde, Cecile  APPLICANT: Counde, Cecile  APPLICANT: Counde, Cecile  APPLICANT: Capron, Andre  ITILE OF INVENTION: RHil6 Polypeptide and its Fragments and Polymucleotides Encoding  TITLE OF INVENTION: RHil6 Polypeptide and Therapeutic Uses  TITLE OF INVENTION: RHIL6 POLY-1-12  PRIOR APPLICATION NUMBER: PCT/FR01/01411  PRIOR APPLICATION NUMBER: PC00-65-11  PRIOR APPLICATION NUMBER: PC00-65-11  NUMBER OF SEQ ID NOS: 56  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 10  LENGTH: 1443  TORANISM: Homo sapiens  FEATURE:  LOCATION: 927  LOCATION: 927  LOCATION: 927  COURT INFORMATION: n = A,T,C or G  QUERY MATCH: 143;  MATCHES LASS MAILARITY 99.7%; Pred. NO. 0;  MATCHES 1438; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  MATCHES 1438; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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2696 ATGAGACAGTTAATGATTTCCGAGAGAAGATGATGTATAAAAGCTATACATTGTGTTCAAA 2755
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                      DB 16; Length 1392;
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                                                77; Indels
                    Score 1278.8; DB 10
Pred. No. 1.1e-288;
); Mismatches 77;
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                      38.0%;
94.1%;
                        Query Match
Best Local Similarity 94.1
Matches 1311; Conservative
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              ACTICIAGAAATAATGACAAGGATTCAAACTTATTGTCAAATGAGTCCAATGTCAGATTT
                            Sequence 48, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
Sugan G. Stuart
Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: VGNKnown>
FILING DATE: AUKNOWN>
FILING DATE: AUKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 97,071
REFERENCE/DOCKET WUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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TELEFAX: (650) 845-4166
N FOR SEQ ID NO: 48:
NCE CHARACTERISTICS:
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STRANDEDNESS: sing
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CLONE: 004700
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0y         2996         AAAACAAAGACTGCAAAAGAAGTGTGCCGACTATCAAATAAAT	PESULT 12  US-10-275-822A-7  Sequence 7, Application US/10275822A  Sequence 7, Application US/10275822A  Sequence 7, Application US/10275822A  Sublication No. US2040086500A1  Sublication No. US2040086500A1  APPLICANT: Cabron, Andre  TITLE DF INVENTION: Baid Polypeptide and its Fragments and Polymucleotides Encoding  TITLE OF INVENTION: Said Polypeptides and Therapeutic Uses  FILE REPRENEUR 107751-710 OF 1

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                                                                           TITAAAATACTATCAGTTAAACATTTAATATGATTATGATTAATGTATTCATTATGCTAC 3324
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publication No. US20040005579A1

publication No. US20040005579A1

GENERAL INPORMATION:

TITLE OP INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA133P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR PILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: PatentIn Ver. 3.1

LENGTH: 609
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Best Local Similarity 98.6%; Pred. No. 1.5e-124;
Matches 573; Conservative 7; Mismatches 1;
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; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-69
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LOCATION: (600)..(601)
OTHER INFORMATION: n equals
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US-10-264-049-69
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| Sequence 811, Application US/10106698
| Publication No. US20030109690A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide PILE REFERENCE: PA005P1
| CURRENT APPLICATION NUMBER: US/10/106,698
| CURRENT FILING DATE: 2000-03-27 |
| PRIOR FILING DATE: 2000-09-28 |
| PRIOR FILING DATE: 1999-09-29 |
| PRIOR FILING DATE: 1999-09-29 |
| PRIOR FILING DATE: 1999-09-29 |
| PRIOR FILING DATE: 1999-06-29 |
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| PRIOR FILING DATE: 1999-06-39 |
| PRIOR FILING DATE: 1999-06-30 |
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Similarity 98.6%; Pred. No. 1.5e-124;
73; Conservative 7; Mismatches 1;
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (600)... (601)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (606)... (606)
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Matches 573, Conservative
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ORGANISM: Homo sapiens
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WESULT 18.

WESULT 18.

Sequence 25, Application US/10228897

PUD10221 NO. US20030092043A1

GENERAL INFORMATION:

APPLICANT: Fisher. Paul B.

APPLICANT: Gopalkrishnan, Rahul V.

APPLICANT: Gopalkrishnan, Rahul V.

ITILE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED

TITLE OF INVENTION: GENE-5 AND PROMOTER AND USES THEREOF

FILE REFERENCE: A4614-A-PCT-USA (070050.2121)

CURRENT APPLICATION NUMBER: US/10/228,897

CURRENT PILING DATE: 2002-08-26

PRIOR PILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-29

NUMBER: OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 6406
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Matches 556, Conservative
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; ORGANISM: homo sapiens
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835621 MA wollf08.x x108h12.x 707909 MA xf76b02.x xo12b12.x 603173580 7p08d10.x

Fri

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AK037057

Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930105B04 product:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens], full insert
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Sciurognathi; Muridae; Murinae; Mus.
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Nature 409, 685-690 (2001)
                                                                              A1718277
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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Mus musculus
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S Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Haramoto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Hayatsu,M., Hiraoka,T., Hiroka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,A., Ohno,M., Ohazto,N., Okazaki,Y., Saito,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sagabe,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Direct Submission

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Broyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science In Mouse Genome

Broyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken

Divasion of Experimental Animal Research in Riken contributed to

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/db_xref="GI:26331914"
/translation="MSIVGSAEDSFRNLILFFRPRLKMYIQVEPVLDHLIFLSAETKE
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NSNMGRDSGTMGSDSDESVIQTKRVSPEPELQLRPYQMEVAQPALDGKNIIICLPTGS
GKTRVAVYITKDHLDKKKQASESGKVIVLVNKVMLAEQLFRKEFNPYLKKWYRIIGLS
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
224. .>2302
                        Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2304)
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similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5
[Homo sapiens] (SPTR|Q9H3G6, evidence: FASTY, 75.6%ID,
67.6%Hongth, match=2079)"
Consortium and the RIKEN Genome Exploration Research
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9930105B04"
/db_xref="taxon:10090"
/clone="9930105B04"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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41.4%; Score 1393; DB 3; Length 2304; ilarity 79.3%; Pred. No. 0; Conservative 0; Mismatches 435; Indels 7

Query Match Best Local Similarity Matches 1691; Conserv

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                                                                               GACAATTGAAGACAGAAACCGGATTGCTGCTGCAGAAAAAAATGGAAATGAATCAGGTGT
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// protein ide "BAC30614.1"

// db_xref="GI:26333793"

// tranlateino="WalvCaABBDERNLILFFRPRILKWYIOVEPVLDHLIFLSAETKE

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SHLETFYTDEKEKKKFAVLNDSDKSDDEASSCNDQLKGDVKKSLKLDETDBFLWNLFFD

N.
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
1.231
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                                                                                                                                                                                                                                                                                                                                    similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens] (SPTR [09H3G6, evidence: FASTY, 75.6%ID, 67.6%length, match=2079)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACATTCAGGTGGAGCCAGTGCTGGACCACCTCATCTTTCTCTGCAGAAACCAAAGA
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                                                                                                                                                                                                                                                                                                                   enriched
                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
/db_xref="texon:10090"
/db_xref="texon:10090"
/clone="A430105A06"
/tissue_type="thymus"
/clone="thymus"
/clone="thymus"
/dev_stage="0 day neonate"
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ilarity 79.2%;
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                                                                                                                                                                                           Length 1013;
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18 I (Bases I to 1013)

19 II (Bases I to 1013)

20 Inguilsehed (1999)

31 Contact: Robert Strausberg, Ph.D.

32 Email: cgapbs-r@mail.nih.gov

71ssue Procurement: ATCC

33 Contact: Robert Strausberg, Ph.D.

34 Email: cgapbs-r@mail.nih.gov

71ssue Procurement: Life Technologies, Inc.

35 Contact: CDNA Library Preparation: Life Technologies, Inc.

36 Contact: Agencourt Bioscience Corporation

36 Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

36 Clone distribution: MGC Clone distribution information can be http://image.llnl.gov

37 Plate: LLAM12875 row: g column: 07

38 High quality sequence stop: 721.

38 Location/Qualifiers
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BQ233683.1 GI:20415083
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TTATTGTCAAATGAGTCCAATGTCAGATTTTGGAACTCAACCTATGAACAATGGGCCAT 1916
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                CTGGTGGACAAGCTTCTAGTTAGAGACGTCTTGGATAAGTGCATGGAGGAGGAACTGTTG
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                                                      ACCTTGGAGAAGGGAGTCTGGCACCTTGGTTGGACTCGGGAATTCGTGGAGGCCCTCCGG
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1 (Jabase 1 to 1174).

1 (Jabase 1 to 1174).

1 Unpublished (1999).

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/Link at:

http://image.lln.gov; f column: 06

High quality sequence stops 808.
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AGENCOURT 10127740 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6502757
5., mRNA sequence.
                                           CACCTACGTCCTGGTTGCTCACAGTGGTTCAGGAGTTATCGAACATGAGACAGTTAATGA 2711
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TCTCGTCA-CAATGAAATAGCCATGGTCCAGGCCCGTGGTCGAGCCAGAGCTGATGAGAG
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870 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8949486 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472264
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                TATCAGTTAAACATTTAATATGATTATGATTAATGTATTCATTATGCTACAGAACTGACA 3334
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                                                                                                                                                                                                           /mol_type="mRNA"
/db xref="taxon:9606"
/clone="lnAGE:6472264"
/tissue type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC 71"
/note="Organ: uTerus; Vector: pCMV-$PORT6; Site_1: Not1:
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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1 (bases 1 to 870)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14005 row: o column: 17
High quality sequence stop: 738.
Location/Qualifiers
                                                    CAAAGAAACAATACAAAAAGTGGGGTAGAATTACCTATCACATTTCCCAATCTTGACTATT
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larity 98.4%; Pred. No. 1.8e-184;
Conservative 0; Mismatches 9; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        812
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Homo sapiens
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                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov
Tissue Procurement ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bisscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Rlage: LLAM12216 row: n column: 21

High quality sequence stop: 690.

Location/Qualifiers

1. 1115

/ Organism="Monus Rapiens"
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                            NITH-MGC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Homo sapiens"
/do xref="taxon:9606"
/dlb xref="IMAGE:61734948"
/clone="IMAGE:61734948"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
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found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM13546 row: a column: 17 High quality sequence stop: 556.
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11arity 97.5%; Pred. No. 1.7e-166;
Conservative 0; Mismatches 13;
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 918)
II (bases 1 to 918)
III (bases 1 to 918)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 TCCTGGTTGCTCACAGTGGGTTCAGGAGTTATCGAACGTGAGACTTAATGATTTCCGA
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                        ATGAGTATTGTGATGATGAAGATGAGGATGATTTAAAGAAACCTTTGAAACTGGATG
                                        2180 AAACAGATAGATTTCTCATGACTTTATTTTTTGAAAACAATAAAATGTTGAAAAGGCTGG
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695 TCGAACATGAGACAGTTAATGATTTCCGAGAGAAGATGATGTATAAAGCTATACATTGTG 636
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/organism="Homo sapiens"
/mol_type="mrRNa"
/db xref="texon:9606"
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/clone="DH10B (Life Technologies)"
/clone lib="Worl CGAP FBO"
/nore="Worlor: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site." BCOR I; Site.2: Not I; NCI CGAP FBO a cDNA library containing the following tissue(s): a pool of 3 chondrosarcoma cell lines (grade 2) The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an BCOR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) la tail. The sequence tag for this library is CGCTACGGAC. The cell lines was provided by Dr James Martin of University of Iowa.
TAG IISBUR=Human grade 2 chondrosarcoma cell line pool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Bento Soares, bento-soares@uiowa.edu
POLYA-Yes.
                                                                                                                                                                              BQ772836
UI-H-FE0-bbn-c-04-0-UI.81 NCI CGAP FE0 Homo sapiens cDNA clone
UI-H-FE0-bbn-c-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2630 GTCGAGCCAGAGCTGATGAGAGCACCTACGTCCTGGTTGCTCACAGTGGTTCAGGAGTTA 2689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2690 TCGAACATGAGACAGTTAATGATTTCCGAGAGAAGATGATGTATAAAGCTATACATTGTG 2749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 755)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                   4; Indels . 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 755;
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Pred. No. 3.3e-164;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_LIB=UI-H-FE0
TAG_SEQ=CGCTACGGAC"
                                                                                                                                                                                                                                                   BQ772836
BQ772836.1 GI:21981312
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Best Local Similarity 99.3%;
Matches 731; Conservative (
                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
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                                                                                                                                     RESULT 8
BQ772836/c
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AUTHORS
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276

156

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396

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Enteryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1035)

1 (Dases 1 to 1035)

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Mational Institutes of Health, Mammalian Gene Collection (MGC)

1 Onpublished (1999)

1 Contact: Robert Strausberg, Ph.D.

2 Email: cgapba-remail.nih.gov

1 Issue Procurement: David N. Louis, M.D.

2 Contact: Robert Strausberg, Ph.D.

3 Contact: Robert Strausberg, Ph.D.

4 Contact: Robert Strausberg, Ph.D.

5 Contact: Robert Strausberg, Ph.D.

6 Contact: Robert Strausberg, Ph.D.

7 Contact: Robert Strausberg, Ph.D.

8 Contact: Robert Strausberg, Ph.D.

8 Contact: MGC

7 Contact: Robert Strausberg, Ph.D.

8 Contact: MGC

8 C
BF337464 1035 bp mRNA linear EST 22-NOV-2000 602035195F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183126 5', mRNA sequence.
BF337464
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/db_xref="laxaon:9606"
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/clone_lib="NHH MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_l: Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                            BF983236 173-JAN-2001
602305873F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397083 5',
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                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 729)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arco
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the IIM.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM10097 row: a column: 20
High quality sequence stop: 665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886 ATGGAGAATAACTCATCAGAATCATCTTTTGCAGATTCTTCTGTAGTTTCAGAATCAGAC
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                                                                                                                                                                        GI:12386048
                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                         mRNA sequence.
                                                                                                                                                                           BF983236.1
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TITLE
JOURNAL
COMMENT
                           RESULT 10
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                                                                   1. .1035
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Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAATGTGGCAGCAAGAGCATCCCCGGAGCCAGAACTCCAGGCTCAGGCCTTACCAAATGG 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTTGCCCAGCCTTGGAAGGGAAGAATATCATCATCTGCCTCCCTACAGGGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAAATCCTTGAAAACTCCCTCTTAAACTTGGAAAATGGAGAAGATGCTGGTGTTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.1%; Score 711.6; DB 2; Best Local Similarity 97.2%; Pred. No. 2e-162; Matches 756; Conservative 0; Mismatches 19;
quality sequence start: 5 quality sequence stop: 695. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049
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Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is Martin from the University of Iowa.

TAG TISSUE-Human grade 2 chondrosarcoma cell line pool TAG_LIB=UI-H-FEI TAG_ECGCTACGGAC.
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                                                                                                                                                                                                                                                                                                              19.4%; Score 654.4; DB 6;
llarity 99.0%; Pred. No. 1.8e-148;
Conservative 0; Mismatches 4;
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Tunoir Gene Index.

Tunoir Gene Index.

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Entribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu
                                                                                                                                                                                                                                                                 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1246 ATAGITCTIGICAATAAGGIACTGCTAGTTGAACAGCTCTTCCGCAAGGAGTTCCAACCA 1305
                                                                                                                                                                      GITTACATTGCCAAGGATCACTTAGACAAGAAAAAAAGCATCTGAGCCTGGAAAAGTT 1245
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                                   ACAAGTTTGGCAGAAGGAAGTGTCAGCTGCTTAGATGAAGTCTTGGACATAACAGCAAC 420
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/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: BcoR I;
Site_2: Not I; NCI CGAP_FEI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed accorning to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 701)
NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                           421 ATGGGCAGTGATTCAGGCACCATGGGAAGTGATTCAGATGAAGAAATGTGGCAAGAAGA
                                                                                                                                                                                                    1006 ATGGGCAGTGATTCAGGCACCATGGGAAGTGATTCAGATGAAGAGAATGTGGCAGCAAGA
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Homo sapiens
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CA423868/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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/clone="INAGE:4304805"
/tissue_type="leiomyosarcoma cell line"
/tissue_type="leiomyosarcoma cell line"
/lab host="DH108 (phage-resistant)"
/clone line="MIH MGG 46"
/clone line="MIH MGG 46"
/clone line="MIH MGG 46"
/note="Organ: uTerus, Vector: pOTB7; Site_1: XhoI; Site_2:
ECRI; cDNA mde by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-eslected >500bp for average insert size
GGCACGAG(G). Size-eslected by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ism Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 781)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapba-romail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM170 row: 1 column: 22

High quality sequence stop: 731.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF686405 11 22-DEC-2000 602143786F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304805 5', mRNA sequence.
                                                                                                                                                         1077 GCCAGAACTCCAGCTCAGGCCTTACCAAATGG--AAGTTGCCCAGCCAGCCTTGGAAGGG
                                                                                                                                                                                                                                                            719 AAGACTATCATCATCTG-CTCCCTACAGGGAGTGGAAAAACAGAAGTGGCTGATTACATT
                              AAGGAAGTGTCAGCTGCTTAGATGAAAGTCTTGGA - CATAACAGCAACATGGGCAGTGAT
                                                               540 AAGGAAGTGTCAGCTGCTTAGATGAAAGTCTTGGACCATAACAGCAACAACAGGGGCAGTGAT
                                                                                                                             1018 TCAGGCACCATGGGAAGTGATTCAGATGAA-GAGAATGTGGCAGCAAGAGCATCCCCGGA
                                                                                                                                                                                                                                                                                                                            135 AAGAATATCATCATCTGCCTCCCTACAGGGAGTGGAAAAACCAGAGTGGCTGTTTACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       778 AGCCACGGATCACTTAGACAAGAACAAAGAACATCTGAGCCTGGAACAG 827
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Pred. No. 7.9e-148;
0; Mismatches 2;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.4%;
Matches 675; Conservative (
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BF686405
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S NHH-MGC http://mgc.nci.nih.gov/.

INTH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM10630 row: b column: 06
High quality sequence stop: 763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="lazon:psec"/
/db_xref="lazon:psec."/
/db_bost="IMAGE:4776869"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skn1; Vector: pcMv-SPORT6; Site_1: Not1;
/note="Organ: skn1; Vector: pcMv-SPORT6; Site_1: Not1;
/site_2: sali; cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCAGCCCTCTGGCCGCCCGCTACATGAACCCTGAGCTCACGGACTTGCCCTCTCCATC
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                                                                          Craniata; Vertebrata; Butele
Catarrhini; Hominidae; Homo.
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19.4%; Score 652.8; DB 4;
Best Local Similarity 96.1%; Pred. No. 4.6e-148;
Matches 798; Conservative 0; Mismatches 17;
                                             Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 827)
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                            sapiens (human)
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BX492926

DKF2781C0628 rl 781 (synonym: hlcc4) Homo sapiens cDNA clone DKF27781C0628 5', mRNA sequence.

BX492926.1 GI:32004887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxn":506"
/clone="IMAGE:5555523"
/clone="Type="leiomyosarcoma"
/lab host="DHIDB (phage-resistant)"
/clone=lib="NIH MGC_71"
/clone=lib="NIH MGC_71"
/clone=lib="NIH MGC_71"
/clone=lib="NIH MGC_71"
/clone=lib="NIH MGC_71"
/clone=lib="NIH MGC_71"
/cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb.
                                                                                                                                                                                                                                                                                                                                                                                                                              TIGCCCTCTCCATCGTTTGAGAACGCTCATGATGAATATCTCCAACTGCTGAACCTCCTT 531
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                                                                                                                                                                                                                                                                                                                             Gapa
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                                                                                                                                                                                                                                                                                            Length 1046;
                                                                                                                                                                                                                                                                                                                            15, Indels
                                                                                                                                                                                                                                                                                        Score 626; DB 4; L
Pred. No. 1.7e-141;
0; Mismatches 15;
                     04
http://image.llnl.gov
Plate: LLAM12275 row: n column:
High quality sequence stop: 622.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        tch 18.6%;
al Similarity 97.7%;
635; Conservative
                                                                   1. .1046
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1046)

SNH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: cgapbs-r@mail.nih.gov

Tassue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM476961 1046 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6481569 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555523
5', mRNA sequence.
BM476961
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                                                                   CGCTACATGAACCCTGAGCTCACGGACTTGCCCTCTCCATCGTTTGAGAACGCTCATGAT 504
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                                                                                                                                GAATATCTCCAACTGCTGAACCTCCTTCAGCCCACTCTGGTGGACAAGCTTCTAGTTAGA
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/db xref="taxon.9606"
/db xref="taxon.9606"
/dc srage="adult"
/lab_host="DH10B"
/clone lib="781 (synonym: hlcc4)"
/note="woctor: pSportl_Sfi; Site_1: SfilB; cDNA-collection"
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                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 627)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5. sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dKEz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKEZp781C0628) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERNANNY; Email: clone@rzpd.de.
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MIPS
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Search completed: January 27, 2005, 17:52:21 Job time : 9214 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: January 26, 2005, 19:38:26; Search time 165 Seconds
(without alignments)
2228.470 Million cell updates/sec
Perfect score: 5311
Sequence: 1 MSNGYSTDENFRYLISCFRA......LPITFPNLDYSECCLFSDED 1025
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries

A Geneseq\_23Sep04:\*

1: geneseqp1990s:\*

2: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2003s:\*

6: geneseqp2003s:\*

7: geneseqp2003s:\*

8: geneseqp2003s:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aael0155 Human mel	Adj75424 Marker ge	Adn04880 Antipsori	Aam47798 Human RNA	Adc31794 Human nov	Aae10165 RNA helic	Adj76213 Marker qe	_	Ada54899 Human pro	Aau23647 Novel hum	Aam40129 Human pol	Aam41915 Human pol		Abp69672 Human pol	Human	Aau00296 Interfero	Aau00298 Interfero	Adj70225 Human hea	Adf76335 Novel hum	Adi75428 Marker de	Marker	Antipsc	Adm05830 Human pro	Aau00297 Interfero	Aau00299 Interfero
SUMMARIES	AAE10155	ADJ75424	ADN04880	AAM47798	ADC31794	AAE10165	ADJ76213	AAU23090	ADA54899	AAU23647	AAM40129	AAM41915	ADC33339	ABP69672	AAB93708	AAU00296	AAU00298	ADJ70225	ADF76335	ADJ75428	ADJ75495	ADN04860	ADM05830	AAU00297	AAU00299
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## ALIGNMENTS

AAE10155 standard; protein; 1025 AA.

RESULT 1 AAE10155 ID AAE1 XX AC AAE1 XX DT 29-N

(first entry)

AAE10155; 29-NOV-2001

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DE	E Human melanoma differentiation associated (Mda)-5 protein.	
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                            The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IrN) inducible gene with structural similarities to RNA helicases and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the artileukaemic compound mezerain (MEZ). Mda-5 is useful for identifying compounds that may induce its expression. Mda-5 is useful for treating compounds that may induce its expression. Mda-5 is useful for treating cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer of the central nervous system and aspecially where the cancer is a cancer of the central nervous system and apoptosis. The Mda-5 promoter exhibits melanocyte tissue specificity and minimises systemic toxicity.
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ive 0; Mismatches
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ry epithelial cell; interleukin-13; respiratory; antiasthmatic;
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cc stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an inducer that induces bronchial asthma in a mouse; (5) a cathod for producing an animal model for bronchial asthma in a mouse; (5) a cathma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial occid corresponding to a portion of asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene through an RNAi effect or an antibody recognising cc a protein encoded by a marker gene; and (7) a DNA chip for testing for expression of the gene through an RNAi effect or an antibody recognising cc a protein encoded by a marker gene; and (7) a DNA chip for testing for concontain asthma or chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory cc and antisathmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for the bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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900 900 The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention. GIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRT IEHETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNP IEHETVNDFREKMYKAIHCVQNWKPESYAHKILELQMQSIMEKKMKTKRNIAKHYKNNP Wood WI; GIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRT ICKCGQAWGTWMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKMVELPITFPNLDYSECCL 'n : acid or polypeptide, useful for preparing a composition for diagnosing or treating psoriasis Length 1025; Williams PM, antipsoriatic; gene therapy; psoriasis; diagnosis. ., 8 Schoenfeld J, B ID NO 1274; 3069pp; English. ġ Antipsoriatic protein sequence #620. ADN04880 standard; protein; 1025 Jackman J, 2002US-0414006P. 25-SEP-2003; 2003WO-US030907.

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                                                                                                      Human; RH116; RNA helicase; cytostatic; virucide; anti-HIV; immunosuppressive; immunostimulatory; antirheumatic; antiarthritic; antiartericosclerchic; osteopathic; antidiabetic; hepatrotropic; antiinflammatory; cancer; infection; HIV; hepatitis; genetic disease; autoimmune disease; graft rejection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, useful for treating and diagnosing cancer or inflammation, and drug screening, comprises a human polynucleotide homologous to RNA helicase.
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The invention relates to 971 novel human CDNA sequences (ADC29919-ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinent production of a polypeptide of the invention; an antibody gainst a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The invention methods for the identification of compounds that modulate the and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modulate the expression or activity of the polymclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention or activity of the polympetides encoded by the contigs (ADC32629) and the polypeptides encoded by the contigs (ADC33861-ADC33627) and the polypeptides encoded by the contigs (ADC33629). The nucleic acids and polypeptides of the invention are activity of data and products dependent on DNA and amino acid sequences. They are disease and other neurodegenerative diseases, anemia, platelet cancer. The nucleic acids may also be used as Mybridiabation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as anemia, platelet and as folds when polypeptide sequence of the invention. Note: The sequence cancer also useful in electronic format date of the printed specification, but sequences of the printed specification, but sequences of the printed specification, but sequences of the printed specification, format date for this patent did not form part o
                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
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Ma Y, Asundi V,
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2; Mismatches
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The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IFN) inducible gene with structural similarities to RNA helicase and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the antileukaemic compound mezerain (MEZ). Mda-5 is useful for identifying compounds that may induce its expression. Mda-5 is useful for reating compounds that may induce its expression. Mda-5 is useful for reating cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer of the central nervous system and especially where the cancer is a cancer of the central nervous system and apoptosis. The Mda-5 promoter exhibits melanocyte tissue specificity and minimises systemic toxicity.
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                                                Human; melanoma differentiation associated gene; Mda-5; interferon; IFN; RNA helicase motif; caspase recruitment domain; CARD; therapy; melanoma; neuroblastoma; astrooytoma; glioblastoma; multiforme; cancer; cervical; breast; colon; prostate; osteosarcoma; chrondosarcoma; systemic toxicity; central nervous system; cytostatic; apoptosis.
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respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are stimulated with interleukin-13. Also described: (l) a group of genes (S2) whose expression levels decrease when respiratory epithelial colls are stimulated with interleukin-13. Also described: (l) a reagent (l) for stimulated with interleukin-13. Also described: (l) a reagent (l) for colls are screening for a candidate compound for a therapeutic agent (c) a kit for screening for a candidate compound for a therapeutic agent (c) a kit for screening for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of cont
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79.6%; Pred. No. 9.1e-316;
ive 75; Mismatches 132; Indels
                                            Claim 16; SEQ ID NO 1465; 241pp; English.
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Matches 817; Conservative
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07-JUN-2000; 2000US-021946FP

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07-JUL-2000; 2000US-02168B0P

11-JUL-2000; 2000US-021748PP

11-JUL-2000; 2000US-021748PP

11-JUL-2000; 2000US-021748PP

11-JUL-2000; 2000US-021748PP

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11-JUL-2000; 2000US-021748PP

14-JUL-2000; 2000US-021748PP

14-JUL-2000; 2000US-021748PP

14-JUL-2000; 2000US-021748PP

14-JUL-2000; 2000US-021748PP

14-JUL-2000; 2000US-022514PP

14-JUL-2000; 2000US-0225214PP

14-SEP-2000; 2000US-0225214PP

14-SEP-2000; 2000US-02231414PP

14-SEP-2000; 2000US-02231414PP

14-SEP-2000; 2000US-0223141PP

14-SEP-2000; 2000US-0233164PP

14-SEP-2000; 
      IICKCGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDXSECC 1019
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AIADATREDPFKEKLLEIMTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKKGNRKERV
                                                             CAEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDED
                                                                                                                        EDDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESA
                                                                                                                                                                                PSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIVRENKALQKKCADYQINGE
                                                                                                                                                                                                                                                                                                                                                                                                                       RGIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFR
                                                                                                                                                                                                                                                                                      TGKINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSG
                                                                                                                                                                                                                                                                                                                                               VIEHETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human enzyme polypeptide #176.
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2000US-018062BP.
2000US-018464P.
2000US-0189874P.
2000US-0190076P.
2000US-0190776P.
2000US-019123P.
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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18-APR-2000;
19-MAY-2000;
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isomerases or ligases. The sequences of the invention are useful in

diagnosis, treatment, prevention and/or prognosis of a wide range of isorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AlDS) autoimmune disorders (e.g. cancer), arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. inflammatory disorders of the invention can also be used in gene therapy. AAU22915-AAU33814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from WIPO at

886888888888888888888888

Sequence 558 AA;

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Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 1086; 1180pp;
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2000US-0249210P.
2000US-0249211P.
2000US-0249212P.
2000US-0249213P.
                                                                         2000US-0246476P.
2000US-0246477P.
2000US-0246478P.
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2000US-0246528P.
2000US-0246532P.
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2000US-0246525P.
2000US-0246526P.
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2000US-0249245P.
2000US-0249264P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                  SEPGKVIVLVNKVLLVBQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIIST
                                                       294 ENVAARASPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKA
                                                                             ENVAARASPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKA
                                                                                                              SEPGKVIVLVNKVLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIIST
                                                                                                                                                                    AQILENSLLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKK
                                                                                                                                                                                   AQILENSLINLENGEDAĞVQLSDFSLIIDECHHTNKEAVYNNIMRHYLMQKLKANNRLKK
                                                                                                                                                                                                                        ENKPVIPLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQ
                                                                                                                                                                                                                                         ENKPVIPLPQILGLTASPGVGGATKQAKAEHILKLCANLDAFTIKTVKENLDQLKNQIQ
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                                Gape
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 Length 558;
                              16; Indels
48.9%; Score 2595.5; DB 4; 94.6%; Pred. No. 3.9e-192; iive 10; Mismatches 16;
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              Best Local Similarity 94.6
Matches 510; Conservative
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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases,

Homo sapiens

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AAU23647 standard; protein; 417 AA
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or diseases in
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C, Irie R, Tamechika I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGRINLLIATTVAEEGLD
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                                                                                                                                                                                                                                                                                                                New polynucleotides encoding full-length polypeptides, e.g. secreto: and/or membrane proteins, useful for developing medicines for disean which the gene is involved, or as target molecules for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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99.1%; Pred. No. 2e-181;
tive 2; Mismatches 2; Indels
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                                                                                                                                                                                                      Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID NO 2467; 205pp; English.
                                                                                                                                                      (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                        14-SEP-2001; 2001JP-00328381
24-JAN-2002; 2002US-0350435P
                                                                             21-MAR-2002; 2002EP-00006586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.1
Matches 464; Conservative
                                                                                                                                                                                                    Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                   WPI; 2003-395539/38.
N-PSDB; ADA53260.
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                EP1293569-A2
                                             19-MAR-2003
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RESULT 10 AAU23647

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Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autofimmune disorder; euclofimmune disorder; enzological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                              Novel human enzyme polypeptide #733
                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000; 2000US-0179065P.

24-FEB-2000; 2000US-0186464P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189814P.
17-MAR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
10-JUL-2000; 2000US-021515P.
11-JUL-2000; 2000US-021644P.
11-JUL-2000; 2000US-021684P.
11-JUL-2000; 2000US-021684P.
11-JUL-2000; 2000US-021888P.
11-JUL-2000; 2000US-021888P.
11-JUL-2000; 2000US-02188P.
11-JUL-2000; 2000US-02188P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
14-AUG-2000; 2000US-0225214P.
16-AUG-2000; 2000US-0225344P.
11-SEP-2000; 2000US-0229314P.
11-SEP-2000; 2000US-0229314P.
11-SEP-2000; 2000US-0229314P.
11-SEP-2000; 2000US-0229314P.
11-SEP-2000; 2000US-0239314P.
11-SEP-2000; 2000US-0239344P.
                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US001239
                                                                                                                                                                                                                                                 nephrotropic; anticoagulant
                                                                          (first entry)
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PR 08-5EP-2000; 2000US-0232091P.
PR 14-5EP-2000; 2000US-0232399P.
PR 14-5EP-2000; 2000US-023239P.
PR 14-5EP-2000; 2000US-023239P.
PR 14-5EP-2000; 2000US-023340P.
PR 14-5EP-2000; 2000US-023340P.
PR 14-5EP-2000; 2000US-023349P.
PR 25-5EP-2000; 2000US-02349P.
PR 25-5EP-2000; 2000US-024417P.
PR 25-5EP-2000; 2000US-0244517P.
PR 25-5EP-2000; 2000US-024451P.
PR 25-5EP-2000; 2000US-024451P.
PR 25-5EP-2000; 2000US-024451P.
PR 25-5EP-2000; 2000US-024951P.
PR 25-5EP-2000; 200
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67

4; Gaps

35.0%; Score 1860; DB 4; Length 417; 90.8%; Pred. No. 2.9e-135; iive 13; Mismatches 20; Indels

Query Match Best Local Similarity 90.8' Matches 365; Conservative 621

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742 EKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKEC 801

PR 01-DEC-2000; 2000US-0255019E.

PR 01-DEC-2000; 2000US-0255019E.

PR 05-DEC-2000; 2000US-025103E.

PR 05-DEC-2000; 2000US-025103E.

PR 05-DEC-2000; 2000US-025103E.

PR 05-DEC-2000; 2000US-025105E.

PR 06-DEC-2000; 200US-025105E.

PR 06-DEC-2000S.

PR 06-DEC-2000S.

PR 06-DEC-2000S.

PR 06-DEC-2000S.

PR 06-DEC-2000S.

PR 06-DEC-2000S.

PR 06-DEC-200S.

PR 06-DEC-20

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22-OCT-2001

AAM40129

RESULT 11 AAM40129 26-JUL-2001

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MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVL 913
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                                                                                                                                                          RFLMTLFFENNKKLKRLAENPEYENFKLTKCRNTIMEQYTRTEESARGIIFTKTRQSAYA
                                                                                                                                                                                                                                    LSQWITENEKFAEVGVKAHHLIGAGHSSEFKPWTQNEQKEVISKFRTGKINLLIATTVAE
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                                                                                                                                                                                                             LSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
                                                   Length 356;
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Yang Y,
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                                                 Score 1839; DB 4;
Pred. No. 9.6e-134;
0; Mismatches 2;
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00663191.
19-OCT-2000; 2000US-00663191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
                                                 34.68;
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                                                                                      Matches 350; Conservative
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                                                                     Local Similarity
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              Sequence 356 AA;
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                                                 Query Match
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Wang D;
, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral solerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren F, Wa
Zhang J,
                                                                                      NIVIRYGLVTNEIAM-VQARGRARADESTYVLVAHSGSGVIE 842
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Yang Y,
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Xue AJ,
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rman T, Xu C,
Drmanac RT;
                                                                                                                                                                                                     AAM40129 standard; protein; 356 AA
                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 3274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-00488725
2000US-00552317
2000US-00598042
2000US-00620312
2000US-00653450
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2000US-00727344
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Wehrman T,
                                                                                                                                                                                                                                                                                   (first entry)
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
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19-OCT-2000;
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25-APR-2000;
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wang D; Zhao QA;

Ren F, Wa Zhang J,

WO2003029271-A2.

Homo sapiens.

N-PSDB; AAI61071

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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, themoteatic/chemokinetic activity, haemostatic
                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                 invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                         Example 2; SEQ ID NO 6846; 10078pp; English.
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ö 739 859 919 979 ENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIK 799 122 182 242 62 680 FFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIFTKTRQSAYALSQWIT 63 ENEKFAEVGVKAHHLIGAGHSSEFKFWTQNEQKEVISKFRTGKINLLIATTVAEEGLDIK ECNIVIRYGLVINEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDPREKMMYKAIH CVQNMKPEEYAHKILELQMQSIMEKKWKTKRNIAKHYKNNPSLITFLCKNCSVLACSGED CVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSGD IHVIEKMHHVNMTPEFKELYIVRENKALQKKCADYQINGEIICKCGQAWGTMMVHKGLDL Gaps ; 33.3%; Score 1769; DB 4; Length 348; 97.4%; Pred. No. 2.5e-128; PCLKIRNFVVVFKNNSTKKOYKKWVELPITFPNLDYSECCLFSDED 1025 PCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED 348 Indels Pred. No. 2.5e-128, 2; Mismatches 7: Best Local Similarity 97.4 Matches 337; Conservative 123 920 243 980 Query Match 740 800 860 303 ઠે 엄 ò 셤 ð 셤 8 요 ઠે 셤 8 g

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Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antinflammatory; cytostatic;
                                                                                                                               Human novel contig-encoded polypeptide sequence, SEQ ID NO:3421.
ADC33339 standard; protein; 348 AA.
                                                                                   (first entry)
                                                                                      18-DEC-2003
                                                                                                                                                                                                                                                                                                                         gene therapy
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ENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIK 122 ENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIK 799

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The invention relates to 971 novel human CDNA sequences (ADC29919-CC ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nuclaic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; and methods of against a polypeptide of the invention; and methods of invention further discloses methods of the invention; and methods of invention further discloses methods of polymelecting or polypeptides of the invention. The invention is medical condition; kits comprising polynucleotide probes and or monclonal antibodies for rarying out the methods of the invention or activity of the journal compounds that modulate the expression or activity of the polymelectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are expression or activity of the polymelectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are expression of matching and polypeptides of the invention are useful in diagnostics, days screening, foremsics, gene mapping, in the identification of mutations responsible for genetic disorders or other traitie, for assessing biodiversity, and in producing many other types of data and other neurodegenerative diseases such as Parkinson's disease, Alzhaimer's diseases and other neurodegenerative diseases, namemia, placatel the cancer. The nucleic acids may also be used as hybridisation probes or primers, and other neurodegenerating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contigener also useful in generating antibodies, as molecular weight markers, and the the recombinant production of a prototic. The sequence data for this patent disouse, as molecular with the present sequence represents a human contigener as also useful in generating anti
                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
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                                                                                                                                                                                                                                                                           Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                         Wang J,
Wang Z, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1769; DB 7;
Pred. No. 2.5e-128;
                                                                                                                                                                                                                                                       , Zhao QA,
ABundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 3421; 1185pp; English.
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2; Mismatches
                                                                                                                                                                                                                                                         Xue AJ,
Ma Y, A
                                                                                                                                                                                                                                                       Tang TY, Zhang J, Ren F, Xv
Zhou P, Ghosh M, Wang D, Ms
Haley-Vicente D, Drmanac RT;
                                                                                                                          24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                  24-SEP-2001; 2001US-0324631P
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                                                                                                                                                                                                                                                                                                                                         WPI; 2003-371981/35.
N-PSDB; ADC32572.
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                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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                                                                                  10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
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AAB93708 standard; protein; 678
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                                                                                                                                                                                                                                                                           426
                                                                                    Sequence
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                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative diseases (parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
                919
                                                                                 242
                                                                                                            979
                                                                                                                                                                                                                                                                                                                                                                              cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; disbetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F;
ECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKMMYKAIH
                                                      CVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSGED
                                                                           CVQNWKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSGED
                                                                                                          IHVIEKMHHVNMTPEFKELYIVRENKALQKKCADYQINGEIICKCGQAWGTMMVHKGLDL
                                                                                                                              IHVIEKWHHVNMTPEFKELYIVRENKTLQKKCADYQINGEIICKCGQAWGTWMVHKGLDL
                                                                                                                                                                                                                                                                                                                                                                   genome mapping; gene therapy; food supplement; virus; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao QA,
                                                                                                                                                              PCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED 1025
                                                                                                                                                                              PCLKIRNFVVVFKANSTKKQYKKWVELPITFPNLDYSECCLFSDED 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1719; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ich RW, Asundi V, Zhe
Yamazaki V, Chen R,
g D, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 1719.
                                                                                                                                                                                                                                                          standard; protein; 678
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J. Wang D,
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T, Wang J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABZ11889
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                         123
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platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                         425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 KPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIF 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AERRLLALFDDRKNELAHTATHGP-ENPKLEMLEKILQRQFS-SSNSPRGIIF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKTROSAYALSOWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRIGKIN 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 VHLVTQ-HGEEFRRMLDGRWTVTTLSGDMGPRAGFGHLARCHDLLICTAELLQMALTSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 SQDPFGDLLKKLMDQIHDHLEMPELSRKFGTQMYBQQVVKLSEAAALAGLQBQRVYALHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGEDAGVOLSDFSLIIIDECHHTNKEAVYNNIMRHYLMOKLKNNRLKKENKPVIPLPQIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 REDPFKEKLLEIMTRIQTYCQMSPMS-DFGTQPYEQWAIQMEKKAAKKGNRKERVCAEHL
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                  Length 678;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                            Match 25.5%; Score 1352; DB 5; 1 Local Similarity 40.7%; Pred. No. 1.6e-95; les 292; Conservative 136; Mismatches 237;
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length CDNAs defined in the specification. Where a primer set comprises:

[a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence, where the comprises a teast 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH13612 to AAH13612 represent thuman amino acid sequences; and AAH13612 to AAH13612 represent in the are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDWAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                       Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 13299; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                       Saito K,
Otsuki
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Wakamatsu A, Nagai K,
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Sugiyama T, Wakamats
                                                                                                                                                                              29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300233.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                   28-JUL-2000; 2000EP-00116126
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                                                                                                                                                                                                                                                                                                                                                                       Isogai
Homo sapiens
                                             EP1074617-A2
                                                                                        07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                            Ishii S,
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306 LQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK 365 366 VLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLE 425 426 NGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIPLPQIL 485 GLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKKFAIADAT 545 52; Gaps DB 4; Length 678; Query Match 25.3%; Score 1344; DB 4; Length 6 Best Local Similarity 40.6%; Pred. No. 6.8e-95; Matches 291; Conservative 136; Mismatches 238; Indels 486 116 셤 ð 셤 ઠ 요 ð

Sequence 678 AA;

784 SODPFGDLLKKLMDQIHDHLEMPELSRKFGTQMYEQQVVKLSEAAALAGLQEQRVYALHL 284 RKYNEALQINDIIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLK 664 665 KPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIF 724 LLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHE 844 TVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLIT 904 FLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELY-IVRENKALQKKCADYQINGEIICK 963 REDPFKEKLLEIMTRIQTYCQMSPMS-DFGTQPYEQWAIQMEKKAAKKGNRKERVCAEHL 604 -CGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECC 1019 TKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKIN 225 605 285 374 785 434 845 905 323 725 964 ઠે 요 8 g ò 유 g ò a 셤 ò 셤 ò

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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1154, Ap
Sequence 296, App
Sequence 29, Appli
Sequence 29, Appli
Sequence 15035, A
Sequence 15035, A
Sequence 5, Appli
Sequence 15035, A
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Sequence 1260, Ap
Sequence 4571, Ap
Sequence 5465, Ap
Sequence 9, Appli
Sequence 1, Appli
Sequence 4820, Ap
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Sequence 34, Appl
Sequence 31, Appl
Sequence 1252, Ap
Sequence 11, Appl
Sequence 6, Appli
                                                                     January 26, 2005, 20:07:35 ; Search time 42 Seconds (without alignments) 1618.475 Million cell updates/sec
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-408-020-66
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28	171.5	3.2	2285	m	US-09-308-375-2	Sequence	2, Appli
29	171	3.2	1401	4	US-09-750-590-2	Sequence	2, Appli
30	170	3.2	905	4	US-09-248-796A-16333	Sequence	16333, A
31	167.5	3.2	1132	4	US-09-248-796A-15026	Sequence	15026, A
32	167.5	3.2	1219	4	US-09-107-532A-6020	Sequence	
33	167	3.1	677	4	US-09-328-352-4365	Sequence	4365, Ap
34	167	3.1	3696	m	US-09-134-001C-5080	Sequence	5080, Ap
35	166.5	3.1	1886	m	US-08-938-105-3	Seguence	3, Appli
36	166	3.1	810	4	US-09-248-796A-20281	Sequence	20281, A
37	166	3.1	1937	4	US-09-538-092-918	Sequence	918, App
38	164	3.1	1354	٣	US-08-685-871-2	Sequence	2, Appli
39	163	3.1	1939	m	US-09-310-187A-1	Sequence	1, Appli
40	162	3.1	1939	4	US-09-538-092-917	Sequence	917, App
41	159.5	3.0	926	m	US-09-134-001C-4452	Sequence	4452, Ap
42	159	3.0	442	4	US-09-489-039A-11770	Sequence	11770, A
43	158	3.0	781	~	US-08-675-631-3	Sequence	3, Appli
44	158	3.0	781	4	US-08-359-316A-3	Sequence	3, Appli
45	158	3.0	781	4	US-09-248-776-3	Sequence	3, Appli
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## ALIGNMENTS

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135 LDKCME-----EELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSAFLNVLRQT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPN-LEKEVWGMENNSSES 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 KNG---GGLPNNGVSDTNSQINSVIT--PQV---IAKETVKENGLQKNGGKRDEFSKEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GDKDRKRARVCSYQSERSNLSGRGHVNNSREGDRFMNRKRTRNWDEAGNNKKKRECNNYR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEP-----ELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVY----IAKDHLDKKK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 KMLS----VFLVPKVPLVYQQAEVIRNQTCFQVGHYCGEMGQDFWDSRRWQREF---- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SNMGSD----SGTMGSDSD----SGTMGSDSD-----EENVAARAS 301
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                   Sequence 2, Application US/09590968B

Patent NO. 6737561

GENERAL INFORMATION:
APPLICANT: Ray, Animesh
APPLICANT: Golden, Teresa Ann
TILLE OF INVENTION: GENE ENCODING SHORT INTECUMENTS AND USES THEREOF
FILE REFERENCE: 176/60581
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,316
PRIOR APPLICATION NUMBER: 60/138,316
PRIOR PILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE PATENTING DATE: 2.1
SEQ ID NO 2
LENGTH: 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFAD-----SSVVSESDTSLAEGSVSCLDE-----SLGHN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 406; DB 4; Length 1909; ilarity 23.0%; Pred. No. 3.4e-25; Conservative 131; Mismatches 271; Indels 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local Simi
Matches 199;
-09-590-968B-2
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KFAIADATREDPFKEKLLEIMTRIQTYCOMSPMS-DFGTQPYEQWAIQMEKKAAKKGNRK 596
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                                                                                                                                                              ERVCAEHLRKYNEALQINDTIRMIDAY--THLETFYNEEKDKKFAVIEDDSDEGGDDEYC 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/09408020
Patent No. 6632937
GENERAL INFORMATION:
APPLICANT: Swanson, Rohart A.
APPLICANT: Schaber, Christa
APPLICANT: Schaber, Christa
TILLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
                                              ----RMIGMTATL----PSEREKADE----IMGTLLSKSIAQRTEDDPDVKPYVQETET
                                                                                                             264 A-----AKPLFTAIRITYALNIFEAHGVTPFLKFCERTVKKKGAGVAE-----
                          478 VIPLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCK
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24.3%; Pred. No. 1.3e-15;
ive 94; Mismatches 207; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/408,020 CURRENT FILING DATE: 1999-09-29 PRIOR APPLICATION NUMBER: 60/102,294 PRIOR FILING DATE: 1998-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Cenarchaeum symbiosum
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Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         303 EP-ELOLRPYOMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIV 361
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APPLICANT: Swanson, Robert A.
APPLICANT: Scaleper, Christa
APPLICANT: Scaleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 503
                                                NNIMRHYLMOKLKNNRLKKENKPVIPLPQILGLTASP-GVGGATKQAKAEBHILKLCANL
                                                                           SLVMSEFYHTTPKDKR------PAIFGMTASPVNLKGVSSQVDCAIKIRNLETKL
                                                                                                                      DAFTIKTVKENLDQLKNQIQEPCKKFAIAD-ATREDPFKEKLLEIMTRIQTYCQMSPMSD
                                                                                                                                                                                          FGTQPYEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTIRMID-----A
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| S50 YKVQQSFLSALQSDERVNFQVDVKFQESYLSEVVSLLQCELLEGAAAEKVAAEVGKPENG
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24.7%; Pred. No. 8.5e-16;.
ive 91; Mismatches 204; Indels 1
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LAYIQSRGRARKPGSDYILMVERGN 779
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Patent No. 6632937
GENERAL INFORMATION:
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Best Local Similarity 24.74
Matches 136; Conservative
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US-09-408-020-66
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                                                                                                                                                                          GKNIIICLPTGSGKTRVAVYIAK------DHLDKKKKASEPGKVIVLVNKVLLVEQL 372
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                                         LAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAARASPEPELQLRPYQMEVAQPALE 321
                                                                                                    LARIEM----ERLRLNEKF------QESQEEIKSLTKERDNLKTIKEALEVKHDQL-
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Patent No. 6753314

BATENT NO. 6753314

APPLICANT: HORMANTION:
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
APPLICANT: MANSFIELD Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1099-04-01

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PRIOR FILING DATE: 2000-02-01
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4.1%; Score 217.5; DB 4; Length 2662;
Best Local Similarity 18.6%; Pred. No. 9.7e-09;
Matches 209; Conservative 185; Mismatches 421; Indels 307;
                                                                                                                                              Sequence 31, Application US/09595684B
Patent No. 6544766
GENERAL INPORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: Vaisberg, Eugeni
APPLICANT: Vaisberg, Eugeni
APPLICANT: Vu, Ming
TITLE OF INVENTION: Human kinesins and methods of prod
TITLE OF INVENTION: Human kinesins with the or INVENTION: Human kinesins ritch of INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2000-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                              PMTQ--NEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGR
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3.8%; Score 202; DB 4; Length 3878;
Best Local Similarity 18.8%; Pred. No. 3.8e-07;
Matches 238; Conservative 179; Mismatches 424; Indels 428;
                                                                                                                                                                                                                                                                                                  904 TFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIVRENK 945
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09914259
Patent No. 649536
GENERAL INFORMATION
APPLICANT: MAKOWSKI, Lee
APPLICANT: Hyman, Paul
FAPPLICANT: Williams, Mark
TILE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT PILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOSTWARE FEELS FREEDOMS: 180
SOSTWARE FREEDOMS: NUMBER OF SEQ ID NOS: 180
                                                                                          1851 QLKKQIKDQSLTLSKLEIENLNI--AQELHENLEEMK
                                                                                                                                  823 ARADESTYVLVAHSGSGVI----
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                            Query Match
4.1%; Score 217.5; DB 4; Length 2663;
Best Local Similarity 18.6%; Pred. No. 9.7e-09;
Matches 209; Conservative 185; Mismatches 421; Indels 307; Gaps
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                                                                                                                                uccation: (0) [.(0) OTHER INFORMATION: Polypeptide Accession Number 002224 US-09-538-092-1252
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version 0.9
SEQ ID NO 1252
                                                                                                                       NAME/KEY: misc_feature
                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PTLVDKL-LVRDVLDK-----CMEEELLTI-EDRNRIAAAENNGNE--SGVRELLKRIVQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 LLSTT-----VQPNLEKEVWGMENNS----SESSFADSSVVSESDTSLAEGS--- 266
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                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BELICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.7%; Score 194.5; DB 1;
llarity 19.2%; Pred. No. 8.3e-07;
Conservative 186; Mismatches 473;
                                                                                                                                                                                                                                                     CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-0CT-193
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
TELEFHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
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                                                                                                                     IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                     Floppy disk
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                                                                          COMPUTER READABLE FORM:
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                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                  MEDIUM TYPE:
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1515 FETVDVKFKEEFKPLSKE----LGEHGKEILLSNSDPHDIPESKDCVLTISEEMFSKDKT 1570
                                                                                                       1987 VQCQAEKVRDDLQKQVKALEIDVEEQVSRPI-ELEQEKNTELMDLRQQNQALEKQLEKMR 2045
                                                                                                                                                                                                          1631 RERVLLEELEALKQLSLAGREKLCCELRNSSTQTQNGNENQGEVEEQTFKEKELDRKPED 1690
                                                                                                                                                                                                                                                                                                                                                                                  2082 ISBHQTREVEQLANHLKEKTDKCSELL---LSKEQLQRDIQERN------EEIEKLE 2129
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                                                                          ---SD 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                            540 AIADATREDPFKEKL-LEIMTRIQTYCQ--MSPMSDFGTQ----PYEQWAIQMEKKAAKK 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       706 NTIMEQYTRIEESARGIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --HETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKR-----NIAKH 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 GNRKERVCAEHLRK--YNE-----ALQINDTIRMIDAYTHLETFYNEEKDKKFAVI--
                                                                                                                                                                                                                                                     -----IMRHYLMQKLKNNRLKKENKPVIPLPQILGLTASPGVGG------
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APPLICANT: Lee, Wen-Hwa
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                     -----ATKQAKABEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKK--
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                                                                     -----DIIISTAQILENSLLNLENGEDAGVQL------
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                                                                                                                                                                   -CHHTNKEAVYNN-
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Sequence 6, Application US/08328254; Patent No. 5710022; GENERAL INFORMATION:
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2291 TDNKVIEEK 2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 BAYVPSSDTYIEKDSSVNDEIDKLRHSATSSLLERNDVIVÍASVSCIFGLGSPFEYQKQV 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 -----EGGDDEYCDGDEDEDDL------KKPLKLDETDRFLMTLFFENNKML 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ALEGKNIIICL-PTGSGKTRVAVYIAKDHLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.6%; Score 193.5; DB 4; Length 661;
Best Local Similarity 18.8%; Pred. No. 1.2e-07;
Matches 147; Conservative 130; Mismatches 240; Indels 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V-----RLKKENKPVIPLP--
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NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...661

SEQUENCE DESCRIPTION: SEQ ID NO: 3677:
US-09-107-532A-3677
                       GTC-012
                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
REGISTRATION NUMBER: 40,489
REFERBENCE/DOCKET NUMBER: GT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GR--KEGE-----
                                                  OMMULAL
TELEPHONE: (781,0277
TEPAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 RASPEPELQLRPYQMEVAQP --
                                                                                                                INFORMATION FOR SEQ ID NO: 3677:
                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                        1915
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                                                  1916 H---QLWKEQNLELRNLTVELEQKIQVLQSKNASLQDTLEVLQSSYKNLENE---LELTK 1969
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                       515 AFTIKTVKENLDQLKNQIQEPCKKFAIADATREDPFKEKLLEIMTRIQTYCQMSPMSDFG
                                                                                                                                                                                                        627 ETFYN------EEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLKKPLKLDETD
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                                                                                                                TQPYEQWAIQMEKKAAKKGNRKERVCA--EHLRKYNEALQIN--DTIRMIDA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION WUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION WUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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STATE: Massachusetts
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COMPUTER READABLE FORM
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US-09-107-532A-3677
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                                                                                                                                                                             ALEGKNIIICLPTGSGKTRVAVYIAK-DHLDKKKKASEPGKVIVLVNKVLLVEQLFRKEF 377
                                                                                                                                                                                                                                                                                                                                                                                                            ------CANLD 514
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                      224 LLSTT------VQPNLEKEVWGMENNS----SESSFADSSVVSESDTSLAEGS---- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----MHHVNMTPEFKELYIVRENKA-----LQKKCADYQINGEIICK
                                                        2142 ALSLTKCELENQIAQLNKEKELLVKESESLQARLSESDYEKLNVSKALEAALVEKGEFAL
                                                                                                  267 -VSCLDESLGHNSNMGSDSGTMGSDSDE-----ENVAARASPEPELQLRPYQMEVAQP
                                                                                                                                                                                                                                                       OPFLKKWYRVIG-----LSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLEN-----
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner. Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
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EHGIVPKTIIKEIRDLISITKESEDDTKEAVQVSYEEMTKEEKDTLLMKLEKEMKDAAKA 641
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                                                                                                                                                                                     Sequence 1, Application US/08353700
Patent No. 559919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATUNER, JERONE B.
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN, TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 3.6%; Score 191.5; DB 1; al Similarity 19.2%; Pred. No. 2.3e-06; 221; Conservative 184; Mismatches 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION UNGREE: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 3248 amino acids
amino acid
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MOLECULE TYPE: protein
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                                                        952 ADYQ 955
                                                                                            LDPE 645
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ORGANISM: HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                       US-08-353-700-1
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Best Local S
Matches 221
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2576 LEKAQLLQGLDEAKNNYIVLQSSVKGLIQEVEDGKQKLEKKDEEISRLKNQIQDQEQLVS 2635
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                                                                                                                                                                                                                                                                                            575 TQPYEQWAIQMEKKAA------KKGNRKERVCAEH-----LRKYNEALQIN--- 614
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Patent No. 6753314

Batent No. 6753314

APPLICANT: INFORMATION:
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REPERENCE: 1596-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1000-01-07

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01
                                                                                                                      -- LGLTASPGVGGATKQAKAEEHILKL
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ORGANISM: Homo sapiens
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INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 RVKMYIQVEPVL-----DYLIFLPAEVKEQIQRIVATSG-----NMQAVELLLS
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      ... rrote:
....wresSE:
....wresSE:
Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.6%; Score 191.5; DB 5; Best Local Similarity 19.2%; Pred. No. 2.3e-06; Matches 221; Conservative 184; Mismatches 465;
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRAER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                 ZIP: 19103-2307
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SWOFTARRE: Patentin Palace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not
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2922 QKTGTVMDTKVDELTTEIKELKETLEEKTKEADEYLDKYCS-LLISHEKLEKAKEMLETQ 2980
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                                                                                                                                               2865 ELKKTYMDNLKYVNOLKKENERAOGKMKLLIKSCKOLB---EEKEILOKELSOLOAAOEK 2921
                                                                                                                                                                                                           ------MHHVNMTPEFKELYIVRENKA-----LQKKCADYQINGEIICKCGQAWGTM 971
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                                                                                            KKMKTK------RNIAKHYKNNPSLITFLCKNCSVLACSGEDIHVIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08685576
; Sequence 4, Application US/08685576
; Patent No. 5906819
; GENERAL INFORMATION:
APPLICANT: Raibuchi, Kozo
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Ita akano, Takeshi
APPLICANT: Ita, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
; TITLE OP INVENTION: RHO TARGET PROTEIN RHO-KINASE
; CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLSY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTIA: COUNTIA: COUNTIA: COUNTIA: CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,576
FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.5%; Score 188.5; DB 2; Best Local Similarity 18.2%; Pred. No. 1.1e-06; Matches 204; Conservative 195; Mismatches 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beat. Stephen A.
REGISTRATION NUMBER: 16887/843
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1388 amino acids
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                                                                                                                                                                          Indels 265; Gaps
                                                                                                                    Length 3210;
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49454
US-09-538-092-1154
                                                                                                                 Query Match
3.6%; Score 189.5; DB 4;
Best Local Similarity 19.1%; Pred. No. 3.4e-06;
Matches 218; Conservative 187; Mismatches 473;
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Sequence 295.429.
Sequence 296.429.
Facent No. 6673549
Facent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Euchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA.0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
FRIOR APPLICATION NUMBER: 60/240,409
FRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHLGWTREFVEALRRTGSPLAARYMNPEL-TDLPSPSFENAHDEYLQLLNLLQPTLVDKL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVRDVLD----KCMEBELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSAFLNVL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESSFADSSVVSESDISL----AEGSVSCLDESL-----GHNSNMGSDS-GTMGSDSD 292
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3.5%; Score 188.5; DB 4;
Best Local Similarity 18.2%; Pred. No. 1.1e-06;
Matches 204; Conservative 195; Mismatches 399;
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US-09-976-594-296
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	QY 647EGGDDEYCDGDEDEDDLKKPLKLDETDRFLMTLFFENNKML 687  DD 920 TKADSEQLARSIAEEQYSDLEKERIMKELEIKEMMARHKQELTEKDATIASL-EETNRTL 978	QY 688 KRLAENPEYENEKUTKLRNTIMEQYTRTEESARGIIFTKTRQSAYALSQWITEN 741	Qy 742EKFAEVGVKAHHLIGAGHSSEFKPMTQNEQXEVISKFRTGKINLL 786           : : :   : :   1   1   1   1	OY 787 -IATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGV 840 : :       :	QY 841 IEHETVNDFREKOMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKN 898  1140 GDAEADDGFPESRLEGWLSLPVRNNTKKFGWVKKYVIVSSKKILFYDSEQDKEQS 1194	QY 899 NPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIVRENKALQKKCADY 954	QY 955 QIN-GEIICKCGQAMGTMMVH974 :	QY 975KGLDLPCLKIRNFVVVFKNNSTKKQYKKWV 1004 : :	សូមស	; APPLICANT: Faris, Mary ; APPLICANT: Turner, Christopher M. ; TITLE OF INVENTION: PROSTATE CANCER MARKERS ; FILE REFERENCE: PA-0036 US ; CURRENT APPLICATION NUMBER: US/09/919,172	CURRENT FI PRIOR APPL PRIOR FILI NUMBER OF	# SOF INWARE: PERL Program # SOE IN NO 29 # LENGTH: 2125 # TYPE: PRT		OS-03-313-1/2-23 Query Match Best Local Similarity 19.6%; Pred. No. 2.6e-06; Matches 214; Conservative 164; Mismatches 375; Indels 337; Gaps 51;	QY 41 EVKEQIQRTVATSGNMQAVELLLSTLEKGVMHLGWTREFVEALRRT 86   : :   :         : :   :           :	OY 87GSPLAARYMNPELTDLPSPSFENAHDBYLQLINLLQPTLVDKLLVRDVLDKCMEE 141

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971 LEKLNETV-FNTVLDKVEETVEISGESLENNEMBKAFFSEIFDNVKGIQENLLTGMFRSI 1029
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591 VAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEEN--VEESVAENVEESVAENVEESVA
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                                                                                                                                                                                                                                                                                                                              Length 1786;
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3.5%; Score 186.5; DB 3;
Best Local Similarity 19.6%; Pred. No. 2.4e-06;
Matches 201; Conservative 152; Mismatches 373;
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1070 -----SSTEGVQETVTEH------VEQNVYVDVDVPAMKDQFLGILNEAGGLKE 1112
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Search completed: January 26, 2005, 20:23:22 Job time : 51 secs Sequence 45372,

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1 MSNGYSTDENFRYLISCFRA......LPITFPNLDYSECCLFSDED 1025
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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SUMMARIES

Sequence 406, App Sequence 9, Appli Sequence 7, Appli Sequence 2467, Ap Sequence 2467, Ap Sequence 234, App Sequence 334, App Sequence 8, Appli Sequence 4515, App Sequence 4515, App Sequence 2, Appli Sequence 2, Appli Description US-10-055-475-2 US-10-228-897-2 US-10-055-475-9 US-10-055-475-7 US-10-094-749-2467 US-10-094-749-2467 US-10-755-889-234 US-10-755-889-234 US-10-055-475-12 US-10-055-475-12 8 Query Match Length 1025 1025 1025 1025 925 925 925 486 487 5311 5311 5311 5307 5289 5289 1087.5 1086.5 1086.5 1040.5 Score Result

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## APPLICANT: Gopalkrishnan, Rahul V.

TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED

TITLE OF INVENTION: GENE-5 AND PROWOTER AND USES THEREOF;
FILE REFERENCE: A34614-A-PCT-USA (070050.2121)

CURRENT APPLICATION NUMBER: US/10/228,897

FRIOR APPLICATION NUMBER: US/10/228,897

PRIOR APPLICATION NUMBER: 99/515,363

PRIOR PLING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

FRIOR EASTERN FASTERN                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0; Matches 1025; Conservative 0; Mismatches 661 721 721 셤 ò ò q

Sequence 2, Application US/10228897 Publication No. US20030092043A1 GENERAL INFORMATION: APPLICANT: Fisher, Paul B. APPLICANT: Kang, Dong-Chul

10-228-897-2

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; ORGANISM: homo sapiens
US-10-055-475-9
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US-10-755-889-406
i Sequence 406. Application US/10755889
i Publication No. US20040171823A1
i GENERAL INFORMATION:
I TILLE OF INVENTION: PATHWAY
i TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1025; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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| Sequence 7, Application US/10055475
| Publication No. US203002285A1
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TYPE: PRT
ORGANISM: homo sapiens
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                                                       Gaps
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                 Length 1025,
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              Score 5307;
Pred. No. 0;
              99.98;
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                                  Similarity
            Query Match
Best Local Simil
Matches 1024; C
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601 AEHLRKYNBALQINDTIRMIDAYTHLETFYNBEKDKKFAVIEDDSDEGGDDEYCDGDEDE	721 GIIFTKTROSAYALSOWITENEKFAEVGVKAHLIGAGHSSEFKPMTONEOKEVISKERT 721 GIIFTKTROSAYALSOWITENEKFAEVGVKAHLIGAGHSSEFKPMTONEOKEVISKERT 721 GIIFTKTROSAYALSOWITENEKFAEVGKAHLIGAGHSSEFKPMTONEOKEVISKERT 781 GKINLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGV	QY         841 IERETVNDFRENOMYAJHGVQNMKPEEYAHKILELQMQSIMEKCMKTKRNIAGHYKNNP 900           Db         841 IERETVNDFRERCMYKAJHCVQNMKPEEYAHKILELQMQSIMEKCMKTKRNIAGHYKNNP 900           QY         901 SLITFLCKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIVRENKALQKKCADYQINGEI 960           Db         901 SLITFLCKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIVRENKALQKKCADYQINGEI 960           Db         901 SLITFLCKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIVRENKALQKKCADYQINGEI 960           OV         961 ICKCQOAMGTMMVHKGLDLPCLKIRNEVVVFKNNSTKKOYKKMVELDTTFPNIDYSECCI, 1020		RESULT 6 US-10-275-822A-2 ; Sequence 2, Application US/10275822A ; Sequence No. US20040086500A1 ; GENERAL INFORMATION: ; APPLICANT: Bahr, Georges ; APPLICANT: Cocude, Cecile ; APPLICANT: Cocude, Cecile	TITLE OF INVENTION: #H116 Polypeptide and its Fragments and Polynucleotides Encoding; TITLE OF INVENTION: said Polypeptides and Therapeutic Uses FILE REFERENCE: 017753-170 FILE REFERENCE: 017753-170 CURRENT APPLICATION NUMBER: US/10/275,822A PRIOR FILING DATE: 2002-11-12 PRIOR FILING DATE: 2001-05-11 PRIOR FILING DATE: 2001-05-11 PRIOR PLING APPLICATION NUMBER: PCT/FR01/0141 PRIOR PLING APPLICATION NUMBER: DCT/FR01/0161	PRIOR FILING DATE: 2000-05-11  NUMBER OF SEQ ID NOS: 56  SOFTWARE: FastSEQ for Windows Version 4.0  LENGTH: 1025  TYPE: PRT  ORGANISM: Homo sapiens	Tu-z/3-82 Query Matc Sest Local Matches 10	Oy 1 MSNGYSTDENFRYLISCFRARVGMYTQVEPVLDYLTFLPAEVKEQIQRTVATSGNMQAVE 60

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479 IPLPOILGITASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKK 538
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|---NLKKGTIP--SLSIFTLMIFDECHNTSKQHPYNMIMFNYLDQKLGGSS------399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LQEEGWFRGFLDALDHAG--YSGLYEAIESWD----FKKIEKLEEYRLLLKRLQPEFKT 116
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20.5%; Score 1087.5; DB 16; Length 925;
Best Local Similarity 31.5%; Pred. No. 6.5e-64;
Matches 328; Conservative 166; Mismatches 361; Indels 185;
                                                                              TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088.465.
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2031
LENGTH: 925
Zhang, Bing
Gibson, Bradford W
Taylor, Steven W.
                                                Taylor, Steven
Glenn, Gary M.
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US-10-408-765A-2031
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46.2%; Score 2456; DB 14; Length 468;
Best Local Similarity 99.1%; Pred. No. 4e-156;
Matches 464; Conservative 2; Mismatches 2; Indels 0
                    APPLICANT: 150NO, YUUKO
APPLICANT: 150NO, YUUKO
APPLICANT: 150NO, YUUKO
APPLICANT: 150NO, YUUKO
APPLICANT: 160, YUUKO
APPLICANT: NAGAI, KEIICHI
APPLICANT: NAGAI, KEIICHI
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAMA, TSUTOWU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
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APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KONJE
FILER REFERENCE: 064335/0160
CURRENT APPLICATION NUMBER: 0750,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
ROFTMARE: PALENTIN VET: 2.1
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
      ISHII, SHIZUKO
KAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-10-094-749-2467
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US-10-408-765A-2031
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602 RDPSNENPKLEDLCFILQEEYHLNPETIT-ILFVKTRALVDALKNWIEGNPKLSFLKPGI 660

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Patin Docket Preview
APPLICANT: CLARK HILLARY
APPLICANT: CLARK HILLARY
APPLICANT: CLARK HILLARY
APPLICANT: SCHORNEBLD, JULK R.
APPLICANT: SCHORNEBLD, JILL R.
APPLICANT: WOL, WILLIAMS, P. MICKEY
APPLICANT: WOL, MILLIAMS, P. MICKEY
APPLICANT: WOL, MILLIAM I.
APPLICANT: WOL, MILLIAM I.
APPLICANT: WOL, MILLIAM I.
APPLICANT: WOL SCHOOSILIONS and Methods for the Treatment of Immune
ITILE OF INVENTION: Related Diseases
TILL REPERBNCE: P1948R1-US
CURRENT APPLICATION WUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LTGRGKTNQNTGMTLPAQKCILDAFKASGDHNILIATSVADEGIDIAQCNLVILYE 716
                                                                                                                                                                                                                                                                                                     582 AIQMEKKA----AKKGNRKERVC-----AEHLRKYNEALQINDTIRMIDAYTHLETFYN 631
                                                                                                                                                                                                                                                                                                                                                                                                            479 IPLPQILGLTASPGVGGATKQAKAEBHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKK
                                                                                                                                                                        400 GPLPQVIGLTASVGVGDAKNTDEALDYICKLCASLDASVIATVKHNLEELEQVVYKPQKF
                                                                                                                                                                                                                                                                                                                             632 EEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLKKPLKLDETDRFLMTLFFENNKMLKRLA
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                                                                         NSLLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPV
                                                                                                                                                                                                                              539 FAIADATREDPFKE-------KLLEIMTRIOTYCOMSPMSDFGTOPYEOW
                                                                                                                                                                                                                                                     692 ENPEYENEKLIKLRNTIMEQYTRIEESARGIIFTKTRQSAYALSQWITENEK--FAEVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809 LVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKMMYKAIHCVQNMKPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869 YAHKILELQMQSIMEKKMKTKRNIAKHY--KNNPSLITFLCKNCSVLACSGEDIHVIEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHVNMTPEFKELYIVRENKALOKKCADYQINGEIIC---KCGQAWGTMMVHKGLDLPCLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        573 NVRAAGFEEIEQD-----
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ORGANISM: Homo sapien
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US-10-370-715B-8
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TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
CURRENT APPLICATION NUMBER: US/10/75,889
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN NOS: 823
SEQ ID NO 234
LENGTH...25
                                     |: : | | | : : | : : : : : | | HYTVLGDAFKECFVSRPHFK-PKQFSSFEKRAKIFCARQNCSHDWGIHVKYKTFEIPVIK 888
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                                                                                                                                                                  YAHKILELOMOSIMEKKMKTKRNIAKHY--KNNPSLITFLCKNCSVLACSGEDIHVIEKM 926
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                                                                                                                                                                                                                                           HHVNMTPEFKELYIVRENKALQKKCADYQINGEIIC----KCGQAWGTMMVHKGLDLPCLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.5%; Score 1086.5; DB 16; Length 925; Best Local Similarity 31.2%; Pred. No. 7.6e-64; Matches 325; Conservative 166; Mismatches 364; Indels 185; Gaps
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                                                                                                                                                                                                                                                                                                                       IRNFVVVFKNNSTKKQYKKW 1003
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889 IESFVVEDIATGVQTLYSKW 908
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                                                                                                                                                                                                                                       Sequence 12, Application US/10055475
Publication No. US2003002285A1
GENERAL INPORMATION:
APPLICANT: Faher, Paul B.
APPLICANT: Rang, Dong-Chul
APPLICANT: Gopalkrishan, Rahul V.
TITLE OF INVENTION: UNSE OF MDA-5 AS AN ANTIVIRAL AND
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
FILE REFERENCE: A44614-A-PCT-USA-A (070050.1921)
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: CGT/US01/06960
PRIOR FILING DATE: 201-02-28
PRIOR FILING DATE: 201-02-28
PRIOR APPLICATION NUMBER: 09/515,363
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 17
SSO_ID NO 12
                                         984 IRNEVVVFKNNSTKKOYKKW 1003
                                                                                               889 IESFVVEDIATGVQTLYSKW 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.3%
Matches 236; Conservative
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                                                                                                                                                                                                                       US-10-055-475-12
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                                                                                                                                                                                                                                                                                                    VWHLGWTREFVEALRRTGSPLAARYMNPELTDLPSPSFENAH--DEYLQLINLLQPTLVD 127
                                                                                                                                                                                                                                                                                                                                                                                                                            KLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQ--KENWFSAFLNVL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 PEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKKASEPGKVIV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 LVNKVLLVEQ---LFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 IPLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 -NSSESSFADSSVVSESDTSLAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAARAS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YS 239
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                                                                                                                                                                              12 RYLISCFRARVKMYIQVEPVLDYLT--FLPAEVKEQIQRTVATSGNMQAVELLLSTLEKG
                                                                                                                                                                                                                       LOEEGWFRGFLDALDHAG--YSGLYEAIESWD-----FKKIEKLEEYRLLLKRLQPEFKT
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                                                                                                                           Gaps
                                                                                                                     Conservative 166; Mismatches 364; Indels 185;
                                                               Length 925;
                                                               DB 17;
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                                                            20.5%; Score 1086.5; DB
31.2%; Pred. No. 7.6e-64
                                                                                        Similarity
US-10-370-715B-8
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              85;
                                            APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION UNMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4515
LENGTH: 487
                                                                                                                                                                                                                  ; Score 1040.5; DB 15; Lengt; Pred. No. 3.6e-61; 90; Mismatches 161; Indels
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; Sequence 13, Application US/10055475
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
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         Sequence 4515, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
                                                                                                                                                                                                                    19.6%;
                                                                                                                                                                                                                                              Matches 234; Conservative
                                                                                                                                                                            ) ORGANISM: Homo sapiens
US-10-108-260A-4515
                                                                                                                                                                                                                                 Similarity
US-10-108-260A-4515
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Sequence 45372, Application US/09864761

Patent No. US20020048763A1

GENURAL INFORMATION:
GENURAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 AGF------DEIEQDL------TQR----FEEKLQELESISIDPS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 VLLVEQ----LFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 NLENGEDAGV--QLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 LPQILGLTASPGVGGATKQAKABEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKKFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 NENPKIRDLCFILQEEYHLNPET-RTILFVKTRALVDALKKWIKENPKLS--FLKPSILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 IADATREDPFKEKLLEIMTRIQTYCQ-------MSPMSDFGTQPYEQWAIQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKKAA----KKGNRKERVC-----ABHLRKYNEALQINDTIRMIDAYTHLETFYNEEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKFAVIEDDSDEGGDDEYCDGDEDEDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGHSSEFKPMTQNEQKEVISKFRTGKIN-LLIATTVAEEGLDIKECNIVIRYGLVTNEI
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                14.8%; Score 788.5; DB 14; Length 514; 37.4%; Pred. No. 3.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                89; Mismatches 178; Indels
CURRENT APPLICATION NUMBER: US/10/055,475
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US01/06960
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        815 AMVQARGRARADES-TYVLVAH 835
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                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: sus scrofa
                                                                                                                                                                                                                                                                                                                                                                       Similarity
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US-09-864-761-45372
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.58
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US-09-864-761-45372
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14.7%; Score 783; DB 9; Length 166;
Best Local Similarity 93.3%; Pred. No. 1.4e-44;
Matches 152; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQPTLVDKLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESG 163
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SEQ ID NO 45372
LENGTH: 166
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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; Sequence 5088, Application US/10106698 ; Publication No. US20030109690A1

RESULT 15 US-10-106-698-5088

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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE REFERENCE: PA005P1 CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR PAPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5088
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (25)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (26)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (28)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (17)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (18)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (11) - OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-5088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
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Sequence
Homo sapi
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhara, K. Methods of testing for bronchial asthma or chronic obstructive pulmonary disease

Patent: EP 1394274-A 156 03-MAR-2004;
                                                                                                                                                                                                                                                                                                                       Sequence
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AX098238 8
BX647917 B
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 156 from Patent EP1394274.
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BC025508
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BC073528
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CQ776474
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AF028963
BC046208
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AK128989
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AX878393
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Location/Qualifiers
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2326
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1250
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Percent Similarity:
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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CQ776470
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AF095844 Homo sapi
AX300832 Sequence
AX017378 Homo sapi
                                                    January 27, 2005, 17:57:32 ; Search time 9394 Seconds (without alignments) 5159.883 Million cell updates/sec
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5311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                             4526729 segs, 23644849745 residues
                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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701   Leuthritysieuk-gasmitrileMerdludinTyrthrängfurdludiuSeralaarg 720   2266   CTIACCAMTTACAMTACATICAGGGCANTACGGANTACGACACACACA 2328   2267   CTIACCAMTTACAMARCCACACAGGGCCANTACGCTTTCCAGGANTACCACACACACACACACACACACACACACACACACAC	Qy         981 CysLeuLysIleArgAsnPheValValValPheLysAsnAsnSerThrLysLysGlnTyr 1000           Db         3109 TGTCTCAAAATAAGGAATTTTGTAGTGGTTTTTCAAAATAATTCAACAAAGAACAATAC 3168           Qy         1001 LysLysTrpValGluLeuProlleThrPheProAsnLeuAspTyrSerGluCysCysLeu 1020           Db         3169 AAAAAGTGGGTAGGATTACCTATCACATTTCCCAATCTTGACTATTCAGAATGCTGTTTA 3228	Qy         1021 PheSerAepGluAep 1025           Db         3229 TTTAGTGATGAGGAT 3243	RESULT 2 AF095844 LOCUS AF095844 LOCUS AF095844 DEFINITION Homo sapiens melanoma differentiation associated protein-5 (MDAS) mRNA, complete cds.

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401 ProGluValValLysSerCysAspileIleIleSerThralaGlnIleLeuGluAsnSer 420	461 TyrLeuMetGlnLysLeuLysAsnAsnAsnAsuLysLysGluAsnLysProVall1ePro 480		21 VallysGluhsnLeuaspGlnLeuLysAsnGlnIleGlnGluProCysLysPheAla 5 	56 18	61 IleGlnThrTyrCy8GlnMetSerProMetSerA8pPheGlyThrGlnProTyrGluGln 5 	581 TrpAlaileGlnMetGluLysLysAlaAlaLysLysGlyAsnArgLysGluArgValCys 600 	601 AlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnIleAsnAspThrIleArgMetIle 620 	621 AspalaTyrThrHisLeuGluThrPheTyrAsnGluGluLysAspLysDysPheAlaVal 640 	641 IlegluaspasperaspgluglyglyaspaspgluTyrCysAspglyaspgluaspglu 660 	AspaspleulyslysproleulysleuaspGluThraspargPheLeuMetThrLeuPhe 68 [	681 PheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnProGluTyrGluAsnGluLys 700 	701 LeuThrLysLeuArgAsnThrIleMetGluGlnTyrThrArgThrGluGluSerAlaArg 720 	721 GlyileilePheThrLysThrArgGlnSerAlaTyrAlaLeuSerGlnTrpileThrGlu 740 	741 ASDGIULYSPheAlaGluValGlyValLySAlaHiSHiSLeuIleGlyAlaGlyHiSSer 760 
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Qy         41 GluValLysGluGlnTleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu 60           Db         289 GAGGTGAAGGACTACAGACGACACTCGGGAACATGCAGGCAG	101 AspleuProSerProSerPheGluAsnalaHisAspGluTyrLeuGlnLeuLeuAsnLeuc 101 AspleuProSerProSerPheGluAsnalaHisAspGluTyrLeuGlnLeuLeuAsnLeu 101	529 [T[		Qy     181 PheLeuAsnValleuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer     200	Oy 201 AspCysSerGluSerAsnalaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 220 	Qy       221 Glugludaleuserthrihardalginproasnieugluiysgluvaltrpglymet       240         Db       829 GAAGAGCAACTTCTTTCAACCACAGTTCAGCCAAATCTGGAGAAGGAGGTCTGGGGGCATG       888	26	snMet 28       ACATG 10	Oy         281 GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla 300           Db         1009 GGCAGTGATTCAGGCACCATGGGAAGTCATTCAGATGAAGAAATGTGGCAAGCAA	nProa       GCCAG	Oy 321 GluGlyLysAanIleIleIleCysLeuProThrGlySerGlyLysThrArgValAlaVal 340	ysvalile 360            AAGTTATA 124	ω -	381 LeulysLysTrpTyrArgVallleGlyLeuSerGlyAspThrGlnLeuLysIleSerPhe 40

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CSGEDTHVIERCHHYNMTTRKKOYKKWUELPITFPNLDYSECCLFSDED"
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                                /mol_type="unassigned DNA"
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                 organism="Homo
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Rhil6 polypeptides and its fragments and polynucleotides encoding said polypeptides and therapeutic uses
said polypeptides and therapeutic uses
Patent: WG 0185555-A 15-NOV-2001;
Istac (FR); INSTITUT PASTEOR DE LILLE (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           GGAAAATCAATCTGCTTATCGCTACCACAGTGGCAGAAGAAGAAGTCTGGATATTAAAGAA
                                                                                                 CysAsnIleValIleArgTyrGlyLeuValThrAsnGluIleAlaMetValGlnAlaArg
                                                                                                                                                          GlyArgAlaArgAlaAspGluSerThrTyrValLeuValAlaHisSerGlySerGlyVal
                                                                                                                                                                          IleGluHisGluThrValAsnAspPheArgGluLysMetMetTyrLysAlaIleHisCys
                                                                                                                                                                                                                                        ATCGAACATGAGACAGTTAATGATTTCCGAGAGAAGATGATGATAAAAGCTATACATTGT
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NAKFAEVGYKAAHLIGAGHSSEVKPMTQTEQKEVISFFRTGEINLLIATTVAEBGGLDI
KECNIVIRYGLVTNEIAMVQARGRARADESTYVLVTSSGSGYTEREIVNDFREGMDI
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Kovacsovics, M., Martinon, F., Micheau, O., Bodmer, J.L., Hofmann, K. and Tschopp, J. Martinon, R. and Tschopp, J. Gresspression of Helicard, a CARD-Containing Helicase Cleaved during Apoptosis, Accelerates DNA Degradation
Curr. Biol. 12 (10), 838-843 (2002)
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| IleCysLysCysGlyGlnAlaTrpGlyThrMetMetValHisLysGlyLeuAspLeuPro
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Sovacsovics, M., Hofmann, K. and Tschopp, J.

Direct Submission

Submitted (24-JAN-2002) Biochemistry, University of des Boverseses 155, Epalinges, VD 1066, Switzerland Location/Qualifiers

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             PheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrGlySer
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Patent: EP 1394274-A 1065 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
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Matches:
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Mismatches:
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                                                              CQ777379 3771 bp DN Sequence 1065 from Patent EP1394274. CQ777379
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                                                                                                                          Mus musculus (house mouse)
Mus musculus
            US-09-515-363C-2 (1-1025) x CQ777379
                                                                                                      CQ777379.1 GI:45380363
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86.94%
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LeuPheSerAspGluAsp
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Query Match:
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RANGCLLLARIVQKENMFSTPELDVLRQTGGGCPENDTDLAASSHRDGP

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KRAYYNNIRRRYLKQKLRANDLKKQNKPAIPLPQIIGLTASPGVGAAKKQSBEARGHIL

NICANLDAPTIKTVKENLGQLKHQIKEPCKKFVIADDTRENPFKEKLLEIMASIQTYC
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Mus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 3771)

S Kang, D.-C. and Fisher, P.B.

Murine homolog of melanoma differentiaion associated gene-5 - a

DEXH group RNA dependent ArPase

L Unpublished

L Unpublished

E 2 (bases 1 to 3771)

S Kang, D.-C. and Fisher, P.B.

Direct Submission

L Submitted (26-APR-2001) Urology, Columbia University, P & S, 630

West 168th, New York, NY 10032, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF374384 3771 bp mRNA linear ROD 02-MAY-2002 Mus musculus strain C57BL/6J melanoma differentiation associated gene 5-like protein mRNA, complete cds.
                                                                                                                            3232 TACAAGAAGTGGGTGGAATTGCCTATCAGATTTCCTGATCTTGACTACTCAGAATACTGC 3291
                                                                                                                                                                                                  3112 ATTATCTGCAAGTGTGGCCAGGCTTGGGGAACAATGATGGTGGTGCAAAAGGTTTAGATTTG 3171
                                                                                                                                                                                                                                                    /note="RNA-dependent ATPase; predicted molecular weight:
2992 ATCCATGTCATTGAGAAGATGCATCATGTCAATATGACACCAGAATTCAAGGGACTCTAC
                                                                                                                                                                     960 IlelleCysLysCysGlyGlnAlaTrpGlyThrMetMetValHisLysGlyLeuAspLeu
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                                              IleHisValIleGluLysMetHisHisValAsnMetThrProGluPheLysGluLeuTyr
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product="melanoma differentiation associated
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                     GTGATTGCTGATGACACCAGAGAAAATCCATTTAAAGAGAAACTTCTAGAAATTATGGCA
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                                                                  560 ArgileGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGlu
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                                                                                                                                                      LeuGluG]yLysAsnIleIleIleIleCysLeuProThrGlySerGlyLysThrArgValAla
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    GluAsnAsnSerSerGluSerSerPheAlaAspSerSerValValSerGluSerAspThr
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SHLAEYTDEKEKKRAVLNDSDKSDDEASSCNDQLKGDVKKSLKLDETDEFLMNLFFD
NKWALKKLAENPEKTRAVLNDSDKSDDEASSCNDQLKGDVKKSLKLDETDEFLMNLFFD
NKKALKKLAENPEKTRALIKLENTILLEGFTRSEESSRGIFFTRTGSTYALSQNIME
NAKFARVGVKAHHLIGAGRSEVKRWTQTEOKEVISRFRTGETNLLIATTVAEGLDI
KECNIVIRYGLVTNEIAMVQARGRARADESTYVLVTSSGSGVTEREINDFREKMYK
AINRVQNKKPERYAHKILELQVQSILEKKMKYKRSISAKQYNDNFSLITLLCKNCSMLV
CSGENIHVIEKNHVVNMTPEFKGLYIVRENKALQKKFADYQTNGEIICKCGQAMGTMM
VHKGLDLPCLKIRNFVVNFKNNSPKKQYKKWVELPIRFPDLDYSEYCLYSDED"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Ctanrini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2540)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlauener, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haish, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bondloo, M.F., Casavan, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyutf, S.,

Arange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Mallahy, S.J., Boask, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Halton, E., Retteman, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, M.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, M.S., Krzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, U., Smallus, D.E.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, M.A., Schein, J.S.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, M.A.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, J., Smallus, D.E.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, J., Smallus, M.S.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, J., Smallus, M.S.,

Butterfield, M.S., Rrzywinski, M.I., Skalaka, J., Smallus, M.S.,

Butterfield, M.S., Schein, J.S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S., J. S.
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Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N.L., Granite,S., Guan,X., Gupta, D., Laric,P.,
Maduzo,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.
3112 ATTATCTGCAAGTGTGGCCAGGCTTGGGGAACAATGATGGTGCACAAAGGTTTAGATTTG 3171
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                                                                      1000 TyrLysLysLrpValGluLeuProlleThrPheProAsnLeuAspTyrSerGluCysCys
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Homo sapiens interferon induced with helicase C domain 1, mRNA (CDNA clone IMAGE:6502757), partial cds.
                                             ProCysteutysIleArgAsnPheValValValPheLysAsnAsnSerThrLysLysGln
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Contact: MGC help desk
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Boquencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/ product="IFIH1 protein"
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/ db_xref="101:50415795"
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/ db_xref="101:30415795"
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                                                             found
                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 174 Row: p Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27886567.
Location/Qualifiers
1. .2540
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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/db_xref="taxon:9606"
/clone="IMAGE:6502757"
/tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
/note="Vector: pCWV-SPORT6"
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/gene="IFIH1"
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/db xref="LocusID:64135"
/db xref="MIM:606951"
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KEYWORDS SOURCE Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof JOURNAL Patent: WO 02068579-A 15038 06-SEP-2002; PEATURES Location/Qualifiers Location/Qualifiers   Authority of humanesion and other uses thereof   Location/Qualifiers   Location/Qualifiers     Authority of humanesion and other uses     Location/Qualifiers     Authority of humanesion and other uses     Authority of humanesion and other uses     Location/Qualifiers     Authority of humanesion and other uses     Authority of humanesion     Autho	Alignment Scores:     8.03e-219	Qy         1 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla         20				201 AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 
Db 1544 ATCATTGATGATGATCACCACAAGAAGAGGTGTATAATAACATGAGGCAT 1603  Qy 461 TyrLeuMetGlnLysLeuLysAsnArgLeuLysLysGluAsnLysProValllePro 480  1604 TATTGATGCAGAAGTTGAAAACAATAGACTCAAGAAGAAACAAAC	Oy 541 IleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGluIleMetThrArg 560	Db 1964 TGGGCCATTCAATGGAAAAAAGGCAAAGGAAATCGCAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAAGAAGGAAGAATAGAGGAAGAA	641   1162 148pAspSerAspGluGyGlyAspAspGluTyCysAspGluAspAspGluAspAspAspGluAspAspGluAspAspGluAspAspAspAspAspAspAspAspAspAspAspAspAspA	701 LeuThriysLeuArgAsnThrileMetGluGlnTyrThrArgThrGluGluSerAlaArg 701 LeuThriysLeuArgAsnThrileMetGluGlnTyrThrArgThrGluGluSerAlaArg 701 Glyll	Oy 741 ABRIGIULYSPREAAGIUVAIGTVAALDYSAATAHISHISLULIGELYALAGIYHISEF 760  Db 2444 AATGAAAATTTGCTGAAGITCAAAGCCAACCATCTGATTGGAGCTGGACACAGC 2503  Oy 761 SerGluPheLysProMetThrGlnAnGluGlnLy8 772  Db 2504 AGTGAGTTCAAACCCATGACAAAAAAAAAAA 2539	KESULI 9 CQ729104 LOCUS LOCUS LOCUS LOCUS ACCESSION CQ729104 CQ729

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KCADYQINGEIICKCGQAWGTWMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKMVELP
ITFPNLDYSECCLFSDED"
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Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arite,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Kumagai,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Okamoto,S., Okitani,R., Kawakami,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nakase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakami,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S., Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1312-3 Yana, Kisarazu, Chiba 292-0812, Japan
Genomics Laboratory; 1312-3 Yana, Kisarazu, Chiba 292-0812,
Benomics Anti-co-jp, Tel:61-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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/ Organism="Nonco sapiens"

/ Ab Xref="taxon:9606"

/ Clone="NT212106855"

/ Cell line="NT212106855"

/ Cell line | Libe: NT212"

/ Note="Cloning vector: pkEl88FL3~mRNA from NT2 neuronal precursor cells treated 2~weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction.~majorly NT2 neuron"

250 . 1656

/ Note="unnamed protein product"

/ Codon start="1"

/ Codon start="1"

/ Drotein id="Bab1141.1"

/ Ab xref="GI:16551654"

/ Lranslation="WTRIOTYCOMSPMSDFGTOPYEOWAIOWEKKAAKEGNBKERVCA

EHLERYNBALOINDTIRDAYTHLEPENNYALIRALBNEYBENEENTHINGOYTRTE

SARGITETTRYREQSAYALSOWITENEKABUGWEVAHIIGAGHSSEFREMTONEOKEVI

SKRTGRINLLIATTVAEEGLDIKECNIVIRYGLIVNEIAMVOARGRARABSSTYULV

AHSGSGVIERETVNDFREKENYXALHEVONNYARERENAKTREN

ARKHYKNNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMYTPEFKELYIVRENKTLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fulimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakanatsu, A., Ishii, S., Yamamotco, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kamda, K., Wagatsuma, M., Takahashi-Fujii, A., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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1. .1776
/organism="Homo sapiens"
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McErran, K.J., Malek, J.A., Gunaratne, P.H., Racharde, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzhy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Youchman, A., Rodrigues, S., Bulkesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.B., Jones, S.J. and Marra, M.A. Schein, J.B., Jones, S.J. and Marra, M.A. Length human and mouse cDNA sequences
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/translation="MASIQTYCQKSPMSDFGTQHYEQWAIQMEKKAAKDGNRKDRVCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-WAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
Email: Gagabba-romail.nih.gov
Tisaue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .2468 '....or: pCMV-SPORT6" /gene="Ifihl" /note="Synonyms: Helicard, Hlcd, MDA5, MDA-5" /db.xref="MGI:1918836" /db.xref="MGI:1918836" /44. .1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
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/db_xref="GI:19343863"
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2468)
Straubberg, R.L., Fedingold, E.A., Grouse, L.H., Derge, J.G.,
Klausuer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 815 AlaMetValGlnAlaArgGlyArgAlaArgAlaAspGluSerThrTyrValLeuValAla 834
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BC025508
BC025508.1 GI:19343862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1321 TGTTCTGGGGAAGATATCCATGTAATTGAGAAAATGCATCACGTCAATATGACCCCGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLeuGlnMetGlnSerIleMetGluLysLysMetLysThrLysArgAsnIleAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201 GAATTACAGATGCAAAGTATAATGGAAAAGAAAATGAAAACCAAGAGAAATATTGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895 HisTyrLysAsnAsnProSerLeuIleThrPheLeuCysLysAsnCysSerValLeuAla
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                                                                                                                                                                                                                                                                  GlyLeuAspIleLysGluCysAsnIleValIleArgTyrGlyLeuValThrAsnGluIle
                                                                                    | IleSerLysPheArgThrGlyLysIleAsnLeuLeuIleAlaThrThrValAlaGluGlu
                                                                                                                                   835 HisserGlySerGlyVallleGluHisGluThrValAsnAspPheArgGluLySMetMet
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ò	ArgPheLeuMetThrLeuPhePheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsn 69	RESULT 13 AX300841	13

LeuGluLeuGlnMetGlnSerlleMetGluLysLysMetLysThrLysArgAsnlleAla 893 GTCTGCTCGGGAGAAAACATCCATGTCATTGAGAAGATGCATCATGTCAATATGACACCA HisLysGlyLeuAspLeuProCysLeuLysIleArgAsnPheValValValPheLysAsn ArgThrGluGluSerAlaArgGlyIleIlePheThrLysThrArgGlnSerAlaTyrAla LeuileGlyAlaGlyHisSerSerGluPheLysProMetThrGlnAsnGluGlnLysGlu CTGATTGGCGCGGGGCACAGCAGTGAAGTCAAGCCCATGACTCAGACTGAACAAAAGAA ValileSerLysPheArgThrGlyLysIleAsnLeuLeulleAlaThrThrValAlaGlu GTCATTAGTAAATTTCGCACTGGCGAAATAAATCTGCTTATCGCTACGACGGTGGCAGAG GluGlyLeuAspIleLysGluCysAsnIleValIleArgTyrGlyLeuValThrAsnGlu 814 IleAlaMetValGlnAlaArgGlyArgAlaArgAlaAspGluSerThrTyrValLeuVal ATAGCCATGGTCCAGGCCCGGGGTCAGCCTGATGAAAGCACGTATGTCCTGGTC 834 AlaHisSerGlySerGlyValIleGluHisGluThrValAsnAspPheArgGluLysMet .269 Accagcagrocorcadoadriaccoaacoodadarrorraardarriccoadadaadaro MetTyrLysAlaIleHisCysValGlnAsnMetLysProGluGluTyrAlaHisLysIle LygHisTyrLygAsnAsnProSerLeuIleThrPheLeuCysLygAsnCysSerValLeu 914 AlaCysSerGlyGluAspileHisValileGluLysMetHisHisValAsnMetThrPro TyrGlnIleAsnGlyGluIleIleCysLysCysGlyGlnAlaTrpGlyThrMetWal TATCAGACCAATGGAGAGATTATCTGCAAGTGTGGCCAGGCTTGGGGAACAATGATGGTG CACAAAGGTTTAGATTTGCCTTGTCTTAAATAAGGAATTTTGTAGTCAATTTCAAAAT AsnSerThrLysLysClnTyrLysLysTrpValGluLeuProlleThrPheProAsnLeu ProGluTyrGluAsnGluLysLeuThrLysLeuArgAsnThrlleMetGluGlnTyrThr AspTyrSerGluCysCysLeuPheSerAspGluAsp 1025 

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	Qy 414 AlaginileleugluasnSerLeuLeuasnLeugluasnGlygluaspalaglyValGln 433	Qy. 434 LeuSerAapPheSerLeullellelleAapGluCysHisHisThrAanLysGluAlaVal 453 	Oy 454 TyrasnasnileMetargHisTyrLeuMetGlnLysLeuLysAsnasnargLeuLysLeuLysFys 473 	Oy 474 GluasnLysProVallleProLeuProGlnIleLeuGlyLeuThrAlaSerProGlyVal 493	Qy 494 GlyGlyAlaThrLysGlnAlaLysAlaGluGluHisTleLeuLysLeuCysAlaAsnLeu 513 	Qy 514 AspalaPheThrIleLysThrVallysGludsnLeudspGlnLeuLysAsnGlnIleGln 533 			Db 1142 CTTCTAGAATAATGACAAGGATTCAAACTTATTGTCAAATGAGTCCAATGTCAGATTTT 1201 Oy 574 GlyThrGlnProTyrGluGlnTrpAlaIleGlnMetGluLy8by8AlaAlaLy8by8Gly 593	Db 1202 GGAACTCAACCTATGAACATGGGCCATTCAAATGGAAAAAAAA	1262	614 AshAspThrileArgMet.leAspAlaryYrnrfisbedolullifile.res.res.rolucid 	634 Lyaaspiysiysphaalavalliegiuaapaspsersspijuvyiyiyapaspyriii 	RESULT 14 BC004031 LOCUS BC004031 DEFINITION MUS musculus interferon induced with helicase C domain 1, mRNA (CDNA Clone INAGE:4495361), partial cds.	ACCESSION BC004031 VERSION BC004031.1 GI:13278455 KEYWORDS ACTROR AND MUSCULLS (house mouse)	_	AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., AUTHORS Klausner R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K., Hobbins, R.F., Jordan, H., Moore, T., Wars, J.I., Wang, J., Hsieh, F.,	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
N Z	_	AUTHORS Bahr, G., Cocude, C. and Capron, A. TITLE Rhilf polypeptides and its fragments an ald polypeptides and therapeutic uses JOURNAL PATENT: WO 0185955-A 10 15-NOV-2001;	S	/mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN	: 8.88e-157 2442.00 tv: 99.38%	s* Mismatches: 3* Indels: Gaps:	뉙	2 AAAGAAACTGGTTCTCTGCATTCTGGAATGTTCTTCGTCAAACAGGAAACAATGA	TATCA 12	Oy 214 GlnValAspGlyProGlnValGluGluGlnLeuLeuSerThrThrValGlnProAsnLeu 233	Qy 234 GlulyaGluValTrpGlyMetGluAsnAsnSerSerGluSerSerPheAlaAspSerSer 253	254 ValValSerGluSerAspThrSerLeuAlaGluGlySerValSerCysLeuAsp 	274 LeuGlyHisAsmSerAsmMetGlySerAspSerGlyThrMetGlySerAspSerAspGlu 	294 GluasnValalaalaargalaSerProGluProGluLeuGlnLeuArgProTyrGlnMet	Qy 314 GluvalalaGinProAlaLeuGluGlyLyBasnileIleIleCysLeuProThrGlySer 333	Qy 334 GIylysThrargValalaValTyrIlealaLysApHisLeuAspLysLysLysLysAla 353	Qy 354 SerGluProGlyLygVallleValLeuValAsnLygValLeuLeuValGluGlnLeuPhe 373	Qy 374 ArgLysGluPheGlnProPheLeuLysLysTrpTyrArgVallleGlyLeuSerGlyAsp 393

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TLLCKNCSMLVCSGENIHVIEKMHYNMTPEFKGLYIVRENKALOKKFADYQINGEII
CKCQAWGTWMYHKGLDLPCLKIRNFVVNFRNNSPKKQYKKWWELPIRFPDLDYSERYC
LYSDED
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GAGGCCAGCAGTTGCAATGACCAACTTAAGGGCGATGTAAAGAAATCTTTGAAACTGGAC
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30
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Conservative:
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Indels:
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Parange, C.C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McEwan, R.D., Mullahy, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worlalo, K.C., Mazny, D.M., Gayt, L.J., Hulyk, S.W., Villalo, K.C., Muzny, D.M., Sodergran, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Sequencing Group at the Stanford Human Genome
DNA Sequencing by: Sequencing School of Medicine, Stanford University School of Medicine, Stanford Human Genome
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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Series: IRAK Plate: 8 Row: k Column: 18.
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ATTVAEEGLD I KECNI VI RYGLVTNEI AMVQARGRARADESTYVLVTSSGSGVTEREI
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Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI CGAP_Lu29" /lab_host="DH10B"
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REFERENCE
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6 Gaps: 0 -515-363C-2 (1-1025) x AR379503 (1-1392)	604 LeuArgLy	3 TTGAGGAAGTACAATGGGCCCTACAAATTAATGACACAATTCGAATGATAGATGCGTAT 62 624 ThristengluThrPheTvrasnGluGluInsbaspLvsIvsPheAlaValileGluAsp 643		644 AspSerAspGluGlyGlyAspAspAspGluTyrCysAspGlyAspGluAspGluAspAspLeu 663	4 9	AAGAAACCTTTGAAACTGGATGAAACAGATTTCTCATGACTTTTTTTT	684 AsniysMetLeuLysArgleuAlaGluAnnProGluTyrGluAsnGluLysLeuThrLys 703 	leudrgdanThilleMetGluGlnTyrThragThrGluGluSerAlaArgGlyllelle 7	TTAAGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCAGCACGAGGAAAAAT	/24 FILE LYBELLE AND THE STATE OF THE STATE	744 PheAlaGluValGlyValLysAlaHisHisLeuIleGlyAlaGlyHisSerSerGluPhe 763		/ow Lybrower interinational interior of the control	784 AsnLeuleulleAlaThrThrValAlaGluGluGlyGlyLeuAspIleLysGluCysAsnIle 803	543 AATCTGCTTATCGCTACCACAGAGAGAAGAGTCTGGATATTAAAGAATGTAACATT 602 804 ValileargTyrGlyLeuValThrAsnGlullealametValGlnalaargGlyArgAla 823		824 ArgAlaAspGluSerThrTyrValLeuValAlaHisSerGlySerGlyValIleGluHis 843	844 GluThrValAsnAspPheArgGluLysMetMetTyrLysAlaIleHisCysValGlnAsn 863 	864 MetLysProGluGluTyrAlaHisLysIleLeuGluLeuGluLeuGlnMetGlnSerIleMetGlu 883 	884 LysLysMetLysThrLysArgasnileAlaLysHisTyrLysAsnAsnProSerLeuile 903 . 	904 ThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGluAspileHisValile 923	GluLysWetHisHisValAsnMetThrProGluPhelysGluLeuTyrIleValArgGlu 9	963 GAGAAAATGCATCACGACAATATGACCCCAGAATTCAAGGAACTTTACATTGTAAGAGAA 1022 944 AsnLysAlaLeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGluIleIleCysLys 963
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Db 838 GTGGCAGAGGAAGGCCTGGATATCAAAGAGTGCAATATTGTTATTCGTTATGGCCTTGTC 897 Ov 811 ThrAsnGlulleAlaMetValGlnAlaArqGlvArqAlaArqAlaAsqGluSerThrTvr 830		Qy         831 ValLeuValAlaHisSerGlySerGlyValIleGluHisGluThrValAsnAspPheArg         850           Db         958 GTCCTGGTCACGGGGGTTACCGAACGGGAATTCTTACCGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACGAATTTCTTACAATTTCTTACAATTTCTTACAATTTCTTACAATTTCTTACAAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTAC	851 GluLysMetMetTyrLysAlaIleHisCysValGlnAsnMetLysProGluGluTyrAla	1018 GAGAAGATGATGTATAAAGCTATTAACCGTGTTCAAAACATGAAACCAGAGGAGTATGCA	OY NIBLYBRIEGHOLINGHOLINGHOLINGHOLINGHOLINGHOLINGHYBRIEGHORINGHYBAIGH BYO  DD 1078 CATAAGATTTGGAAGTGCAAAGGAAGAGAAAGAAAGAAAG	891 AsnileAlaLysHisTyrLysAsnAsnProSerLeuIleThrPheLeuCysLysAsnCys :::	Db 1138 AGCATTGCAAAGCAATACAACGACAATCCATGGTTAATAACACTTGTGTGAAAAATTGT 1197 Ov 911 CarValtanalaCvacarglvGlnaartlaHteValtInGlntvaMatHteHteValtan 920	1198 AGCATGCTCGCTCGGGAGAAACATCCATGTCATTGAGAAGATGCATGTCATT	931 MetThrProGluPheLysGluLeuTyrIleValArgGluAsnLysAlaLeuGlnLysLys	DD 1258 AIGACACCAGAATICAAGGGACICIACATIGIAAAGAAAAAAAAGAAGGACIGGAAAAAGAAA 131/ Qy 951 CysalaaagpTyrGlnIleaanGlyGluileIleCygbygCygGlyGlnalaTrpGlyThr 970	1318	971 MetMetValHisLysGlyLeuAspLeuProCysLeuLysIleArgAsnPheValValVal	DD 15/8 AIGAIGGIGCACAAAAGGITIAGATTIGCCTIGICTIAAAATAAAGAAATTITGIAGICAAT 143/ Qy 991 PheLygabanAanSerThrLygIygGlnTyrLygLygLygTrpValGluLeuProlleThrPhe 1010	1438 TTCAAAATAACTCACCGAAGAAAAACAGTAAAAAAGAGTGGGTGG	Qy         1011 ProasnLeudspTyrSerGluCysCysLeuPheSerAspGluAsp 1025		AR379903 AR379503 1392 bp DNA linear PAT 18-DEC-2003 DEFINITION Sequence 48 from patent US 6607879.		Unclassified. The Cocks, B.G., Stuart, S.G. and Seilhamer, J.J. TITLE Compositions for the detection of blood cell and immunological	regoonse gene expression JOURNAL Patent: US 66078879-A 48 19-AUG-2003; FEATURES Location/Qualifiers source 11392	/organism="unknown" /mol_type="genomic DNA" ORIGIN	Length: Matches:	t Similarity: 94.79% ocal Similarity: 94.79% Match: 39.01%

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OM protein

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3343. .3348
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/product= "Human
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The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Wda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IFN) inducible gene with structural similarities to RNA helicases and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the antileukaemic compound mezerein (WEZ). Mda-5 is useful for identifying contourds that may induce its expression. Mda-5 is useful for reating cancer eg., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, prostate cancer osteosarcoma, chrondosarcoma and especially where the cancer is a cancer of the central nervous system and apoptosis. The Mda-5 promoter is exhibits melanocyte tissue specificity, and minimises systemic toxicity.
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from a subject with the expression level of the gene in a sample from healthy subject.

Claim 1; SEQ ID NO 156; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy cubject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (51) whose expression levels increase when respiratory epithelial cells are etimulated with interleukin-13, or (b) a group of genes (52) whose expression levels decrease when respiratory epithelial cells are stimmlated with interleukin-13. Also described: (l) a reagent (1) for cetimmlated with interleukin-13, or (b) a group of genes (52) a kit for screening for a candidate compound for a therapeutic agent cetimmlated with interleukin-13. Also described: (l) a reagent (i) for cetimmlated asthma or chronic obstructive pulmonary disease; (c) a minducer that induces bronchial asthma in a mouse; (5) a marker gene or an annial model for bronchial asthma or chronic obstructive pulmonary disease; (c) asthma or chronic obstructive pulmonary disease; (c) asthma or chronic obstructive pulmonary disease; (c) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of corresponding asthma or achronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene; on the method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present corresponding or a procession of the gene through an RNAi effect or an antisathmatic activities, and can be used in gene therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present corresponding for or screening for a therapeutic agent invention. 

Sequence 3380 BP; 1153 A; 644 C; 753 G; 830 T; 0 U; 0 Other;

120 LeuGlnProThrLeuValAspLysLeuLeuValArgAspValLeuAspLysCysMetGlu 140 GlualaLeuArgargThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeuThr 100 468 80 40 9 GluValLysGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu AspLeuProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuAsnLeu ArgValLysMetTyrIleGlnValGluProValLeuAspTyrLeuThrPheLeuProAla LeuLeuLeuSerThrLeuGluLysGlyValTrpHisLeuGlyTrpThrArgGluPheVal MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla Length:
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                                                                                        The present sequence is the coding sequence for human RH116. RH116 is a list by protein and has homology to RNA helicases (DEXH box). RH116 and its coding sequence are useful for treating cancer; acute or chronic infections (especially by HIV or heatitis B or C); inherited genetic diseases; (auto)immune diseases (particularly rheumatism, arthritis, arterisoclerosis, esteoporosis and diabates, but many others listed) and opervent graft rejection. RH116 and its coding sequence are also useft for inducting, or increasing, the immune response to a vaccine
                                                                                                                                                                                                                                                                                                                                 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla
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                     New polypeptide, useful for treati
inflammation, and drug screening,
homologous to RNA helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antinflammatory; cytostatic;
     11eCysiysCysGlyGlnAlaTrpGlyThrMetMetValHisLysGlyLeuAspLeuPro
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Haley-Vicente D, Drmanac RT;
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c ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the CDNA sequences of the invention (ADC31384). The nucleic acids and polypeptides encoded by the contigs (ADC31362) and the polynpeptides encoded by the contigs (ADC31364). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the carists, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease. Alzheimer's disease and other neurodegenerative diseases, anemia, platelet diseases or concer. The nucleic acids may also be used as hybridisation probes or primers and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and an second supplements. The present sequence represents a specifically considered human CDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was ftp.wipo.int/pub/published\_pct\_sequences. 

Sequence 3446 BP; 1184 A; 649 C; 772 G; 841 T; 0 U; 0 Other;

Alignment Pred. No.:	Alignment Scores: Pred. No.:	0	Length:	3446
Score:		5285.00	Matches:	1020
Percent	Percent Similarity:	99.71%	Conservative:	2
Best Lo	Best Local Similarity:	99.51%	Mismatches:	n
Query Match:	fatch:	99.51%	Indels:	0
DB:		10	Gaps:	0
US-09-5	US-09-515-363C-2 (1-1025) x ADC30823 (1-3446)	(5) × ADC30823	(1-3446)	
ò	1 MetSerAsı	GlyTyrSerThrAsp	ScludenPheArgTyr	WetSerAsnGlyTyrserThrAspGluAsnPheArgTyrLeuIleSerCysPheArg
ΩP	237 ATGTCGAAT	GGGTATTCCACAGAC	GAGAATTTCCGCTAT	AIGHTEAN THE THE TOTAL THE TOTAL TO THE TOTAL TO
ò	21 ArgvalLy	MetTyrileGlnVal	ValGluProValLeuAsp	21 ArgValLysMetTyrIleGlnValGluProValLeuAspTyrLeuThrPheLeuPro
qq	297 AGGGTGAA	AATGTACATCCAGGTC	sgagccrgrgcrggac	AGGGTGAAAATGTACATCCAGGTGGAGCCTGTGGTGGACTACCTGACCTTTCTGCCT
ò	41 GluValLy	GluGlnIleGlnArc	JThrValAlaThrSer	41 GluValLysGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaVal
Dp	357 GAGGTGAAC	GAGCAGATTCAGAGC	SACAGTCGCCACCTCC	GAGGTGAAGGAGCAGATTCAGAGGACAGTCGCCACCTCCGGGAACATGCAGGCAG
δ	61 LeuLeuLer	SerThrLeuGluLy	sGlyValTrpHisLeu	LeuLeuLeuSerThrLeuGluLy8GlyValTrpHisLeuGlyTrpThrArgGluPhe
q	417 CTGCTGCT	BAGCACCTTGGAGAA	GGAGTCTGGCACCTT	CTGCTGCTGAGCACCTTGGAGAAGGGAGTCTGGCACCTTGGTTGG
δλ	81 GluAlaLe	JArgArgThrGlySe	rProteuAlaAlaArg	GluAlaLeuArgArgThrGlySerProLeuAlaAlaArgTyrMetAsnProGluLeu
qa	477 GAGGCCCT	CCGGAGAACCGGCAG	ccrcraccccccc	GAGGCCCTCCGGAGAACCGGCAGCCCTCTGGCCGCCCGCTACATGAACCCTGAGCTC

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>-	201	AspCysSerGluSerAsnAlaGluIleGluAsnLeuSerGlnValAspGlyProGlnVal 3	220
qq	837	gatricitcagaaagcaatgcagagattgagaattatcacaagttgatggtcctcaagtg	968
ογ	221	GluGluGlnLeuLeuSerThrThrValGlnProAmnLeuGluLygGluValTrpGlyMet ;	240
Д	897	gaagagcaactictitcaaccacagiicagccaaarciggagaaggaggiciggggcaig	926
ð í	241	GluamnamserSerGluSerSerPheAlaAspSerSerValValSerGluSerAspThr 3	260
ga	ָת מ	GAGAATAACICALCAATAACITIIGAAGAATICATAATAACAATAACAAATAACAAATAAAAAAAAAA	
දු දු	261	Sericualagiudiyseryaisercysicuaspdiusericudiyaisasperasmet 	1076
λά	281	GlyserAspserGlyThrMetGlySerAspserAspGluGluAsnValAlaAlaArgAla	300
Db	1077		1136
٥'n	301	SerProGluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeu	320
Д	1137	TCCCCGGAGCCAGAACTCCAGGTCAGGCCTTACCAAATGGAAGTTGCCCAGCCAG	1196
λό i	321	GluGlyLygaAsnileileileileCysLeuProThrGlySerGlyLysThrArgyalAlaVal	340
Ω	1197	GAAGGGAAGAATATCATCTGCCTCCCTACAGGAGTGGAAAAAACCAGAGTGGCTT	0 1
<u>ئ</u> ج	341	341 TyrileAlaLysAspHisLeuAspLysLysLysLysAlaSerGluProGlyLysVallle 360	360 1316
, >	361	ValleuValAsnLvsValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPhe	380
. q	1317	GITCITGICAAIAAGGIACIGCIAGITGAACAGCICITCCGCAAGAGAGITCCAACIII	1376
٨	381	LeulysLysTrpTvrArgValileGlyLeuSerGlyAspThrGlnLeuLysIleSerPhe	400
q <sub>Q</sub>	1377	THGAAGAAATGGTATCGTGTTATTGGATTAAGTGGTGATACCCAACTGAAAATATCATTT	1436
à	401	ProGluValValLysSerCysAspllellellelleSerThrAlaGln11eLeuGluAsnSer	420
qo	1437	CCAGAAGTIGICAAGICCIGIGAIAITAITAICAGIACAGCICAAAICCIIGAAAACICC	1496
à	421	LeuteuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeulle	440
۵	1497	CICITAAACTIGGAAAATGGAAGAAGATGCIGGIGITCAATIGICAGACTITICCTICAIT	1556
λ'n	441	IlelleAspGluCysHisHisThrAsnLysGluAlaValTyrAsnAsnIleMetArgHis	460
Q <sub>D</sub>	1557	ATCATTGATGAATGTCATCACACCAACAAGAAGCAGTGTATAATAACATCATGAGGCAT	161
à	461	TyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLysGluAsnLysProVall1ePro	480
q	1617	TATTTGATGCAGAAGTTGAAAACAATAGACTCAAGAAAGA	1676
λά	481	LeuProGln11eLeuGlyLeuThrAlaSerProGlyValGlyGlyAlaThrLygGlnAla	200
qo	1677	circricadaracridddacraacarrcaccriggrigriggaggggccacgaagcaagcc	173
λά	501	LysalaGluGluHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThrIleLysThr	520
qo	1737	AAAGCTGAAGAACACATTTTAAAACTATGTGCCAATCTTGATGCATTTACTATTAAAACT	179
<b>\</b>	521	VallysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGluProCysLysLysPheAla	540
qq	1797	GITAAAGAAAACCITGAICAACIGAAAAACCAAATACAGGAGCCAIGCAAGAAGITTGCC	185
λά	541	IleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGluIleMetThrArg	260
q	1857	<u>ATTGCAGATGCAACCAGAAGATCCATTTAAAGAGAAACTTCTAGAAATAATGACAAGG</u>	191

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                                                                                                                 GlyLysIleAsnLeuLeuIleAlaThrThrValAlaGluGluGlyLeuAspIleLysGlu
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                                                                                                                                                                                                                                                                                                                                               SerLeulleThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGluAspIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysLeuLysIleArgAsnPheValValValPheLysAsnAsnSerThrLysLysGlnTyr
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                                                                  741 AsnGluLysPheAlaGluValGlyValLysAlaHisHisLeuIleGlyAlaGlyHisSer
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The present invention relates to an isolated nucleic acid encoding a melanoma differentiation associated gene-5 (Mda-5) polypeptide. Mda-5 contains a caspase recruitment domain (CARD) and a RNA helicase motif. Mda-5 is a novel interferon (IFN) inducible gene with structural similarities to RNA helicases and CARD motif containing proteins. Mda-5 is induced during terminal differentiation in human melanoma cells treated with the combination of recombinant fibroblast IFN and the antileukaemic compound mezerein (MEZ). Mda-5 is useful for identifying compounds that may induce its expression. Mda-5 is useful for treating cancer e.g., melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, brondosarcoma and especially where the cancer is a cancer of the central nervous system and appotesis. The Mda-5 proteir exhibits melanocyte tissue specificity and minimises systemic toxicity. The present sequence is shuman Mda-5 protein-related DNA. Note: The present sequence is designated SEQ ID NO:2 in the main body of the specification, and has been represented in a protein formation in the specification, and has been represented in a protein
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is not further
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                                                       Human melanoma differentiation associated gene; Mda-5; interferon; IFN; RNA helicase motif; caspase recruitment domain; CARD; therapy; melanoma; neuroblastoma; astrocytoma; glioblastoma; multiforme; cancer; cervical; bresst; colon; profeste; osteosarcoma; chrondosarcoma; systemic toxicity; central nervous system; cytostatic; apoptosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid sequences encoding a Melanoma Differentiation Associated Gene useful for cancer cell growth suppression, apoptosis and anti-viral activity.
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Matches:
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GluGluLeuLeuThrileGluAspArgAsnArgileAlaAlaAlaAlaGluAsnAsnGlyAsn 160

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GluValLysGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaValGlu LeuLeuLeuSerThrLeuGluLysGlyValTrpHisLeuGlyTrpThrArgGluPheVal 

ArgValLysMetTyrIleGlnValGluProValLeuAspTyrLeuThrPheLeuProAla

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples, where a higher level expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic said sequences may be useful in disgnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                             Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker gene; gene; ds.
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creation a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagant (1) for teating for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an induce in induces bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial cathma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisene nucleic acid corresponding to a portion of the marker gene or an antisene nucleic acid corresponding to a portion of the marker gene or an antisene nucleic acid corresponding to a portion of the expression of the gene through an RNAi effect or an antibody recognising a probe has been immobilised to assay a marker gene. (1) has respiratory cor bronchial asthma or chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory conditions and antisathmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent invention.
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                 2932 CCATCGTTAATAACACTTCTCTGCAAAAATTGTAGCATGCTGGTCTGCTCGCGGAGAAAAC 2991
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ProSerLeulleThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGluAsp 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                          2992 ATCCATGTCATTGAGAAGATGCATCATGTCAATATGACACCAGAATTCAAGGGACTCTAC
                                                                                                                                                                            | IleIleCysLysCysGlyGlnAlaTrpGlyThrMetMetValHisLysGlyLeuAspLeu
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                                                                                                                                                                                                                                       PróCygLeuLys1leArgAsnPheValValValPheLysAsnAsnSerThrLysLysGJn
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                                                                                                                  IleValArgGluAsnLysAlaLeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGlu
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the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU21814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or lygases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autcommune disorders (e.g. arthritis), neurological disorders (e.g. Albamatory disorders (e.g. asthma), cardiovascular disorders (e.g. therbosicals), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polymucleotides of the infections also be used in gene therapy. AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and polynucleotides useful for diagnosing, preventing,
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535 ProCysLysLysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGluLysLeu 554
                                                                                                                                                                Cytostatic, Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTTACTATTAAAACTGTTAAAGAAAACCTTGATCAACTGAAAAACCAAATACAGGAG
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                      SEQ ID
                                               CDNA; 1776
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24-JAN-2002; 2002US-0350435P.
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Seki N, Yoshikawa T,
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P-PSDB; ADA54899.
                                               standard;
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Best Local Similarity:
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AsnArgLysGluArgValCysAlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnIle
                                                                                                                                                                                                                                                                        ArgPheLeuMetThrLeuPheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsn
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                                                          AATCGCAAAGAACGTGTTTGTGCAGAACATTTGAGGAAGTACAATGAGGCCCTACAAATT
                                                                                                                                                  LysAspLysLysPheAlaValIleGluAspAspSerAspGluGlyGlyAspAspAspGluTyr
                                                                                                                                                                                                              CysAspGlyAspGluAspAspLeuLysLysProLeuLysLeuAspGluThrAsp
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The present invention relates to human RH116 (see AAM47798). RH116 is a li6kDa protein and has homology to RNA helicases (DEXH box). RH116 and ists coding sequence are useful for treating cancer; acute or chronic infections (especially by HIV or hepatitis B or C); inherited genetic diseases; (auto)immune diseases (particularly rheumatism, arthritis, arteriosclerosis, osteoporosis and diabetes, but many others listed) and to prevent graft rejection. RH116 and its coding sequence are also useful for inducing, or increasing, the immune response to a vaccine. The
CATTACAAGAATAACCCATCACTAATAACTTTCCTTTGCAAAAACTGCAGTGTGCTAGCC 1320
                                                                                                              GlnIleAsnGlyGlulleIleCysLysCysGlyGlnAlaTrpGlyThrMetWalHis
                                                                                                                             TOTICIGGGGAAGATATCCATGTAATTGAGAAAATGCATCACGTCAATATGACCCCAGAA
                                                                                  TTCAAGGAACTTTACATTGTAAGAGAAAACAAAACACAGAAAGGGAAAAGTGTGCCGACTAT
                                                                                                                                                             LysGlyLeuAspLeuProCysLeuLysIleArgAsnPheValValValPheLysAsnAsn
                                                                                                                                                                            SerThriysLysGlnTyrLysLysTrpValGluLeuProlleThrPheProAsnLeuAsp
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immunosuppressive; immunostimulatory; antirheumatic; antiarthritc;
antiartericosclerotic; osteopathic; antidiabetic; hepatrotropic;
antiinflammatory; cancer; infection; HIV; hepatitis; genetic disease;
autoimmune disease; graft rejection; vaccine; ds.
                     CysSerGlyGludspIleHisVallleGluLysMetHisValAsnMetThrProGlu
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polynucleotide
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                                                                                              ArglysGluhrgValCysAlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnIleAsn
                                                                                                                                                                           AspThrileArgMetileAspAlaTyrThrHisLeuGluThrPheTyrAsnGluGluLys
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                CCATGCAAGAAGTTTGCCATTGCAGATGCAACCAGAGAAGATCCATTTAAAGAGAAACTT
                                     LeuGlulleMetThrArglleGlnThrTyrCysGlnMetSerProMetSerAspPheGly
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                                                                                                                                                      ABRÀTGLYBG1uATGVA1CYBA1aG1uHi SLEUATGLYBTYTÀBRG1uA1aLEUG1NI1E
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20-UJN-2000; 2000US-005620312.
19-UJL-2000; 2000US-0065312.
14-SEP-2000; 2000US-00653191.
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                           QA;
                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such
              Wang D;
, Zhao Q
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              Ren F,
Zhang J
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Yang Y,
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Indels:
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               Xue
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            Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                           central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                      part of the printed specification
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97.01%
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                 Tang YT,
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Zhou P,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642.AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral neuropathy and localised neuropathies and central nervous system diseases, such as parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arncer diseases and inclammation, leukaemias and therapy, drug screening, assays for receptor activity, arncer disease and inflammation, leukaemias and C. C.N. & disease.
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Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                  cytostatic, gene therapy; cancer; /; central nervous system; CNS;
             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateat sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Yang Y,
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Xue AJ,
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rman T, Xu C,
Drmanac RT;
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2000US-00488725.
2000US-00552317.
2000US-00598042.
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2000US-00653450.
2000US-00662191.
2000US-00693036.
                                                                                                                                                                                                                             26-DEC-2000; 2000WO-US034263.
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Wang Z, Wehrman T,
Goodrich R, Drmanac
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P-PSDB; AAM41915.
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25-APR-2000;
20-JUN-2000;
                                                                                              leukaemia; ss
                                                                                                                                Homo sapiens.
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14-SEP-2000;
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29-NOV-2000;
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Zhou P,
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Sequence 1382 BP; 513 A; 217 C; 285 G; 367 T; 0 U; 0 Other;

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Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
1.81e-164	2120.00	98.32%	97.84\$	39.92%	4	
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GlnIleAsnAspThrileArgMetileAspAlaTyrThrHisLeuGluThrPheTyrAsn 631 US-09-515-363C-2 (1-1025) x AAI61071 (1-1382)

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qa	 73 GAAGAGAAA	
ò	2 GluffyrCys	8pGlyAspGluAspGluAspAspLeuLysLysProLeuLysLeuAspGlu 67
අු	3 GAGTATIG	stgatgaacatgaggatgattttaagaaacctttgaaactggatg
රු සි	672 ThrAsp-Arg          193 ACAGATACG	rgpheleumetThrLeuphepheGluasnasnLysMet-LeuLysArgLeuA 691 
ò	AsnP	roGluTyrGluAsnGluLysLeuThrLysLeuArgAsnThr1leMetGl
ΩÞ	GAACACO	CCTAATATGAAAATGAAAAGCTGACCAAATTAAGAAATACCATAATGGAG
ò	1 lnTyrThrA	9ThrGluGluSerAlaArgGly1le1lePheThrLysThrArgGlnSerA .73
ф	3 AATATACTA	ctgaggaatcagcacgaggaataatctttacaaaacacgacaggt
දු දු	731 laTyralaL	LeuSerGinTrpileThrGluAenGluLyePheAlaGluValGlyValLyeA 751 
ò	1 јанівнів	leglyAlaGlyHisSerSerGluPheLysProMetThrGlnAsnGluG 77
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g G	AGA	AGTAAATTTCGCACTGGAAAAATAAATCTGCTTATCGCTACCACAG S
ò	91 alAlaGlu	rGlyLeuValT 81
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ò.		ametValGlnalaArgGlyArgAlaArgAlaAspGluSerThrTyrV 83
Op	3 CCAATGAAA	:CATGGTCCAGGCCCGTGGTCGAGCCAGAGCTGATGAGAGCACCTACG 67
ò	1 alLeuValP	Indian
셤	673 TCCTGGTTG	tcacagtggttcaggagttatcgaacatgagacagttaatgatttccga
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3	אסואסאיסא כ	TOTATRANGCTATACATTGTGTTCANATATGANGCAGAGGAGTATGCTC / A
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ò	al	вНівТугLувАвпАвпРгоSerLeuIleThrPheLeuCysLувАвпСув
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Db	TAG	CCTGTTCTGGGGAAGATATCCATGTAATTGAGAAAATGCATCACGT
λ̈́σ	Prog	luPheLysGluLeuTyrIleValArgGluAsnLysAlaLeuGlnLysLysC 951
qq	CCCCAG	AATTCAAGGAACTTTACATTGTAAGAGAAAACAAAACACTGCAAAAGAA
δλ	AlaAspT	/rGlnileAsnGlyGluileileCysLysCysGl
qq.	CCGACT	atcaaataaatggaaatcatctgcaaatgtggccaggcttgggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 971 novel human cDNA sequences (ADC29919-CDC20889) and the polypeptides they encode (ADC30890-ADC31860). The ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99$ identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody completed or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ampliorating a medical condition; kits comprising polypuciaectide probes and/or monoclonal antibodies for carrying out the methods of the invention or ampliorating methods for the identification of compounds that modulate the comprise sequences corresponding to the converse of the invention or expression or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are contig sequences corresponding to the cDNA sequences of the invention are contiguently in diagnostics, drug screening, forensics, gene mapping, in the contiguence of the invention are contiguently in diagnostics, drug screening, forensics, gene mapping, in the contiguence of the invention are contage. They are contage of the invention are contage. They are also used for treating diseases such as Parkinson's disease. Alzheimer's
  1153 TCAAAAATAATTCAACAAAGAAACAATACAAAAAGTGGGTAGAATTACCTATCACATTTC 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                             Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; mondeular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
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Weng G;
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Wang Z,
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Ma Y, Asundi
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Zhou P, Ghosh M, Wang D, Mi
Haley-Vicente D, Drmanac RT;
                                                                                                                                                                                    ADC32572 standard; cDNA; 1382
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             disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. who.int/pub/published_pct_sequences.
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anaemia, platelet
                                                                                                                                                                                                                               Sequence 1382 BP; 513 A; 217 C; 285 G; 367 T; 0 U; 0 Other;
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407
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Matches:
Conservative:
Mismatches:
Indels:
    and other neurodegenerative diseases,
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98.32%
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39.92%
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                  891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition comprising a plurality of cDNAs, useful for detecting tered expression of genes in an immunological response or for agnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.
                                                                                                                                                                          heLysAsnAsnSerThrLysLysLysLysLysLysTrpValGluLeuProlleThrPheP
AGAAGATGATGTATAAAGCTATACATTGTGTTCAAAATATGAAACCAGAGGAGTATGCTC
                                                                ATATTGCCAAGCATTACAAGAATAACCCATCACTAATAACTTTCCTTTGCAAAACTGCA
                                                                                                                                              etMetValHisLysGlyLeuAspLeuProCysLeuLysIleArgAsnPheValValP
                isLysIleLeuGluLeuGlnMetGlnSerIleMetGluLysLysMetLysThrLysArgA
                                                    snileAlaLysHisTyrLysAsnAsnProSerLeuIleThrPheLeuCysLysAsnCysS
                                                                                                          GTGTGCTAGCCTGTTCTGGGGGAAGATATCCATGTAATTGAGAAATGCATCACGTCAATA
                                                                                                                            etThrProGluPheLysGluLeuTyrIleValArgGluAsnLysAlaLeuGlnLysLysC
                                                                                                                                                                 ysAlaAspTyrGlnIleAsnGlyGluIleIleCysLysCysGlyGlnAlaTrpGlyThrM
                                                                                                                                                                                                                                                     793 ATAAGATTTTGGAATTACAGATGCAAAGTATAATGGAAAAGAAAATGAAAACCAAGAGAA
                                                                                        erValLeuAlaCysSerGlyGluAspIleHisValIleGluLysMetHisHisValAsnM
                                                                                                                                                                                                                       TGATGGTGCACAAAGGCTTAGATTTGCCTTGTCTCAAAATAAGGAATTTTGTAGTGGTTT
                                                                                                                                                                                                                                                                            roAsnLeuAspTyrSerGluCysCysLeuPheSerAspGluAsp 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoarthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cordetecting the altered expression of genes in an immunological cordetecting the invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of CDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected to hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes or comprising a mon-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising an incoarray and a plurality of detectable complexes and a comprising an immunopathology, such as Crohn's disease, asthma, conference of an immunopathology, such as Crohn's disease, asthma, the diagnosis of an immunopathology, such as Crohn's disease, asthma, collecative colitis, hypereosinophilia, irritable bowel syndrome, concearthritis, theumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in the printing a plant of the printing a plant of the printing a plant of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the pr
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Matches:
Conservative:
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Best Local Similarity:
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	Asnicalicality and an analyzed and a specific of the state of the stat	AAGAAGGTCTGGATA	ValileArgTyrGlyLeuValThrAsnGluileAlaMetValGlnAlaArgGlyArgAla	AAATAGCCATGGTCC	ArgalaAspGluSerThrTyrValLeuValAlaHisSerGlySerGlyValIleGluHis	FI'TGCTCACAGTGGTT	GluThrvalAsnAspPheArgGluLysMetMetTyrLysAlaIleHisCysValGlnAsn	NTGATGTATAAAGCTM	MetLysProGluGluTyrAlaHisLysIleLeuGluLeuGlnMetGlnSerIleMetGlu	trtrggarracag,	LysLysMetLysThrLysArgAsnIleAlaLysHisTyrLysAsnAsnProSerLeuIle	SCCAAGCATTACAAG	ThrPheLeuCysLysAsnCysSerValLeuAlaCysSerGlyGluAspIleHisVallle	radccrerrcrede	GluLysMetHisHisValAsnMetThrProGluPheLysGluLeuTyrlleValArgGlu	cagaattcaaggaa	AsniysAlaLeuGlniysEysCysAlaAspTyrGlnIleAsnGlyGluIleIleCysLys	SACTATCAAATAAAT	CysGlyGlnAlaTrpGlyThrMetMetValHisLysGlyLeuAspLeuProCysLeuLys	GTGCACAAAGGCTTA	IleArgAsnPheValValValValPheLysAsnAsnSerThrLysLysGlnTyrLysLysTrp	AATAATTCAACAAAG	ValGluLeuProlleThrPheProAsnLeuAspTyrSerGluCysCysLeuPheSerAsp	CTTGACTATTCAGAA		
	laThrThrValAlaG	cracacacreecac	lyLeuValThrAsnG	GTCTCGTCACCAATC	erThrTyrValLeuv	GCACCTACGTCCTG	BpPheArgGluLysN	ATTTCCGAGAGAAG	luTyrAlaHisLys	AGTATGCTCATAAG	hrLysArgAsnIle	CCAAGAGAAATATT	ysAsnCysSerVall	AAAACTGCAGTGTG	isvalAsnMetThri	ACGICAATATGACC	InLysLysCysAla	PAPAGAAGTGTGCC	rpGlyThrMetMet	GGGGAACAATGATG	/alvalvalPheLys	STAGTGGTTTTCAAA	[]eThrPheProAsn	ATCACATTTCCCAAT		
	AsnLeuLeuIleA	AATCTGCTTATCG	ValileArgTyrG	GTTATCCGTTATG	ArgAlaAspGluS	AGAGCTGATGAGA	GluThrValAsnA	GÁGÁCÁGTTAÁTG			LysLysMetLysT	AAGAAAATGAAAA	ThrPheLeuCysL				AsnLysAlaLeuC		CysGlyGlnAlaT	TGTGGCCAGGCTT	IleArgAsnPhe	ATAAGGAATTTT		GTAGAATTACCTA	GluAsp 1025	GAGGAT 1268
483	784	543	804	603	2	663	844	723	864	783	884	843	904	903	924	963	944	1023	964	1083	984	1143	1004	1203	1024	1263
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2, Appli 1, Appli

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 48, Application US/09023655;
Patent No. 6607879
GENERAL INPORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Osffrey J. Sellhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
INUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STRATE: CALLFORNIA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 94-0001 US
TELECOMMUNICATION INFORMATION:
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
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2, Appli
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-143-576-7
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US-09-590-968B-1
US-08-916-421B-1
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    723 GAGACAGTTAATGATTTCCGAGAGAAGATGATGTATAAAGCTATACATTGTGTTCAAAAT 782
                                                                                                                                                                  843 AAGAAAATGAAAACCAAGAGAAATATTGCCAAGCATTACAAGAATAACCCATCACTAATA 902
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                                                   MetLysProGluGluTyrAlaHisLysIleLeuGluLeuGlnMetGlnSerIleMetGlu
                                                                                   APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Ran, Felyan
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Linel
APPLICANT: Wang, Zhiwei
APPLICANT: Wehman, Tom
APPLICANT: Wehman, Tom
APPLICANT: Wehman, Non 6783969e1
APPLICANT: Wehman, Non
APPLICANT: Pangy Yonghong
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US-09-799-451-771
US-09-799-451-771
Sequence 771, Application US/09799451
FAPELICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Ren, Aidong J.
APPLICANT: Nam, Aidong J.
APPLICANT: Nam, Aidong J.
APPLICANT: Wang, Jinnen Rui
APPLICANT: Wang, Jinnen Rui
APPLICANT: Wang, Jinnen Rui
APPLICANT: Wang, Jinnen
APPLICANT: Wang, Jinnen
APPLICANT: Wang, Jinnen
APPLICANT: Wang, Jinnen
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Sena
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ORGANISM: Homo sapiens
FEATURE:
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Mismatches:
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Matches:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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TYPE: nucleic acid
TYPE: nucleic acid
LENGTH: 1392 base pairs
LENGTH: 0900.03: 1 inear
LIBRARY: HMCINOTO1
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3.92e-145 Length: 2590 1352.00 Matches: 292 59.69\$ Conservative: 136 7: 40.73\$ Mismatches: 237 4 Gaps: 12	ArgProTyrGlnMetGluValAlaGlnProAlaLeuGluGlyLysAsnIle 32	ysasp 	HistouAsplysLysLysLysAaSerGluProGlyLysVallleValLeuValAsnLys 365	GIGCACCIGGIGACCCAGCAIGGIGAGGITCAGGCGCATGCTGGATGGACGCTGG 414  ArgVallleGlyLeuSerGlyAspThrGlnLeuLySIleSerPheProGluValValLys 405  ACCGTGACAACCCTGAGTGGGGACATGGGACCACGTGCTTTGGCCACCTGGCCGG 474		AsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeulle1le1le1leAspGluCys 445    :::   ::	SHISThrashlysGlualaValTyrAshashlleMetArgHisTyrLeuMetGlnLys 465          :::    :::	LeulysAsnAsnArgLeulysLysGluAsnLysProValIleProLeuProGlnIleLeu 485    :::  CTCCAGAGGCCACAG	GlyLeuThrAlaSerProGlyValGlyGlyAlaThrLysGlnAlaLysAlaGluGluHis 505	SLeuCysAlaAsnLeuAspAlaPheThrIleLysThrValLysGluAsnLeu 525 	AspGinLeuLysAsnGinIleGinGluProCysLysPheAlaileAlaAspAlaThr 545	ArgGluAspProPheLysGluLysLeuLeuGluIleMetThrArgIleGlnThrTyrCys 565 :::	GlnMetSerProMetSerAspPheGlyThrGlnProTyrGluGlnTrpAla1leGln 584 :::	isLeu       ACCTG
i NAME/KEY: CDÈ i LOCATION: (190) US-09-799-451-771 Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	US-09-515-363C-2 (1-102) Qy 306 LeuGlnLeu Dh 190 Amgaacriff	326 250 250	346 310 366	258 GIGCACC Qy 386 ArgVall Db 415 ACCGTGA	Qy 406 SerCysA Db 475 TGCCATG	Qy 426 AsnGlyG    Db 535G	Qy 446 HisHisT           589 CACCACA	Qy 466 LeuLysA    :::  Db 649 CTCCAGA	Oy 486 GlyLeuT         Db 682 GGTCTCA	Oy 506 IleLeulysI :::   :::   Db 742 GTCCTGCAGC	Oy 526 AspGlnL      Db 802 CCCCAGC	Qy 546 ArgGlua :::  Db 862 AGCCAGG	Qy 566 GlnMetS :::    Db 922 GAGATGC	Qy 585 MetGlub ::: : Db 982 CTGAGTG

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APPLICANT: Pisher, Paul B.
APPLICANT: Jiang, Hongping
TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH SPECIFICALLY HYBRIDIZE WITH
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING MDA-7 AND PHARMACEUTICAL COMPOSITIER REFERENCE: A34534-A-A (070050.1637)
CURRENT APPLICATION NUMBER: 08/316,537
PRIOR PILING DATE: 1994-09-30
PRIOR FILING DATE: 1994-09-30
PRIOR PILING DATE: 1993-10-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESE FOR Windows Version 4.0
SEQ ID NO 12
LENGTH: 301
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                                                                                                                       536 CysLysLysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeu 555
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63 GCCACGAAGCAAAGCTGAAGAACACATTTTAAAACTATGTGCCTATCTTGATGCA 122
                                                                             123 TTTACTATTAAAACTGTTAAAGAAAACCTTGATCAACTGAAAAACCAAATACAGGAGCA- 181
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Matches:
Conservative:
Mismatches:
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; Sequence 12, Application US/09221268D

; Patent No. 6720408

; GENERAL INFORMATION:
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472.00
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Best Local Similarity:
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                         2089 AAAGTCCGCAGC----ATGCTGCTGGAGACCCCTCAGGGGGGGGATCCAGGCCAAAAAG
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                                                                                                                                                                                                                                                                       Sequence 7, Application US/08143576
Patent No. 5643761
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
APPLICANT: Jiang, Hongping
TITLE OF INVENTION: METHOD FOR GENERATING A SUBSTRACTED
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSES OF THE GENERATED LIBRARY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                          1003 TrpValGluLeuProlleThrPheProAsnLeuAspTyrSerGluCysCys 1019
                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elam PC compatible
COMPUTER: Elam PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,576
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION INFORMATION:
TELEPROCHOCKET NUMBER: 28,678
TELERAX: (212) 977-9550
TELERAX: (212) 664-055
TELERAX: (212) 677-9550
TELERAX: (212) 677-9550
TELERAX: (212) 677-9551
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FENGTH: 301 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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962 GGTTCCAATGAGTTGGTTTATAGGTCAGGGACTTGGGAAGCTGATCATGAAGAGATGTT 1021
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                       -SerSerValValSerGluSer 258
                                                                                                        ------SerAsnMet 280
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                                                                                                                                       ---SerLeuGlyHisAsn-------
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                     245 SerGluSerSerPheAlaAsp-
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APPLICANT: Ray, Animesh
APPLICANT: Golden, Teresa Ann
TITLE OF INVENTION: GENE ENCODING SHORT INTEGUMENTS AND USES THEREOF
FILE OF INVENTION: GENE ENCODING SHORT INTEGUMENTS AND USES THEREOF
FILE OF INVENTION UNMBER: US/09/590,968B
CURRENT APPLICATION NUMBER: 0000-06-09
PRIOR APPLICATION NUMBER: 60/138,316
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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158
316
275
47
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Matches:
Conservative:
Mismatches:
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39.82%
23.64%
7.64%
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Best Local Similarity:
                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                 LENGTH: 6184
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US-09-590-968B-1
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NAME/KEY: misc_feature_
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OTHER INFORMATION: n equals a,
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LOCATION: (98159)..(98159)
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LOCATION: (98239)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (98343)...(98343)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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SEQ ID NO 1
LENGTH: 1664976
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (84812)..(84812)
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LOCATION: (84808)..(84)
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE OF INVENTION: januaschii
FILE REFERENCE: PB275
2662 GGCAAGAAAGCCTGGATCAGACTACATACTCATGGTTGAGAGAAAAT 2710
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                                                                                                                    CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR PPLING TOWNER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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                                           Sequence 1, Application US/08916421B Patent No. 6503729 GENERAL INFORMATION:
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ORGANISM: Methanococcus jannaschii
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	326	1lelleCysLeuProjhrGjySerGjyLysThrArgValAjaValTyrlleAlaLysAsp	345
	1658848	1658848 TGTGTTTTATCGACAGGTTTAGGTAAAACAGCTATTGCTATTTAGTTATAGCAGGT 1658904	1658904
	346	HislenAsplyslyslyslyslysAlaSerGluProGlyLysValIleValLeuValAsnLys	365
	1658905		1658949
	366	ValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPheLeuLysLysTrpTyr	385
	1658950	1658950 AGACCTTTGGTTGAGCAACACTACAGGTTTAAAACAGGTTTTAAACATTGATGAAGAT 1659009	1659009
	386	386 ArgValileGlyLeuSerGlyAspThrGlnLeuLysIleSerPheProGluValValLy8 405	405
	1659010		1659066
λõ	406	406 SerCysAspllellelleSerThrAlaGlnIleLeuGluAsnSerLeuLeuAsnLeuGlu 425	425
	1659067	AAAGGGAAAATCTTTATAGCTACACCACAAGTTATAGAAAACGATATCATA	- 1659117
	426	426 AsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeulleIleIleAspGlu 444	444
	1659118	1659118GCTGGAAGAATAAATGTGGATGAATTTATTTTAT	1659165

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AspleLysGlucysAsnlleVallleArgTyr 807
                                                                                                                                                    ValdinAlaArgGlyArgAlaArgAlaAspGlu 827
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ATTCAGAGGAGATGAGCGATGAGGGAGAA 1660110
                    -----TyrlleValArgGluAsnLysAla 946
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3TGGGAGATTATGTTTTAAGTGATAGGGTAGTT 1660587
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GaaaaatctaaaGaaataaaGgaaGaGa 1660287
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TCAAAAACTGCAGTAAAAGAAGAAACTAAGGAG 1660347
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yspheArgThrGlyLyslleAsnLeuLeulle 787
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NAME/KEY: misc\_feature LOCATION: (855539)..(855539) OTHER INFORMATION: n equals a, t, c, or g FEATURE: NAME/KEY: misc feature LOCATION: (559167)..(559167) OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc feature LOCATION: (779455)..(779455) OTHER INFORMATION: n equals a, t, c, or ö ö ö ö or or or ö ö ö ö ö NAME/KEY: misc feature LOCATION: (319226)..(319226) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc\_feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature LOCATION: (312993)..(312993) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature LOCATION: (779676)..(779676) OTHER INFORMATION: n equals a, t, c, υÌ ΰ ပဲ NAME/KEY: misc\_feature LOCATION: (309418)...(309418) OTHER INFORMATION: n equals a, t, c, FEATURE: misc\_feature LOCATION: (312837)...(312837) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (674435)..(674435) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (741684)..(741684) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (309398)..(309398) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (657081)..(657081) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (713652)..(713652) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (657203)..(657203) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals FEATURE: FEATURE FEATURE: FEATURE

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465 LysLeulysAsnAsnArgLeuLysLysGluAsnLysProVallleProLeuProGln11e 484	485 LeuGlyLeuThrAlaSerProGlyValGlyGlyAlaThrLygGlnAlaLygAlaGluGluGluGluGluGluGluGluGluGluGluGluGluG	1859235 IIAGGAILIAACGGCAICICCAGGI		530AsnGlnIleGlnGluProCysLysPheAlalleAlaAspAlaThrArgGlu 547	1659445 TTAAAAATATTAAAAGATCCTGGAGTTATAAAATTCCATTGCGATGTAAAAAACAAAAAAAGAAAAAAAA		1659537   1659537   1659537   1659537   1659537   1659537   1659537   1659537   1659537   1659537   1659538   1659538   1659538   1659538   1659538   1659591   165959	614 AsnaspThrIleArgMetIleAspAlaTyrThrHisLeuGlu i::::::::::::::::::::::::::::::::::::	628 ThrPheTyrAsnGluGluLysAspLysLysPheAlaValIleGluAspAspSerAspGlu ::::::::::       ::: 1659652 AATTATCCATGCAAAAAAAAAAATCAGCTAAAATCTATTGTTAATGATGAA	648 GlyGlyAspAspGluTyrCysAspGlyAspGluAspGluAspAspLeuLysLysProLeu 667 1659702	668	688 LysArgLeuAlaGluAsnProGluTyrGluAsnGluLysLeuThrLysLeuArgAsnThr 707	708 IleMetGluGlnTyrThrArgThrGluGluSerAlaArgGlyIleIlePheThrLyeThr 727 	728 ArgGlnSerAlaTyrAlaLeuSerGlnTrpIleThrGluAenGluLysPheAlaGluVal 747	748 GlyValLygalaHisHisLeuIleGlyalaGlyHisSerSerGluPheLygProMetThr 767	768 GlnAsnGluGlnLysGluValileSerLysPheArgThrGlyLysIleAsnLeuLeuile 787 
& f	3 & A	8 & 8	\ \text{\tint{\text{\tin}\text{\ti}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tin}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tin}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\ti}\}\tin}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\te\tin}\tint{\text{\text{\text{\text{\text{\text{\text{\text{\texi}\tint{\text{\text{\text{\text{\texi}\tint{\text{\texi}\text{\texi}\tint{\ti}\tint{\text{\texi}\tinz{\text{\texi}\text{\te\	8 8 8	3 & A	8 8 8	43 & 43 43 & 43	k & &	<b>상</b> 점	P Q	, Ag	d G	4G G	S A	S G	- A
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NAME/KEY: misc_feature LOCATION: (871519)(871619) OTHER INFORMATION: n equals a, t, c	NAME/KEY: misc_feature LOCATION: (1084830)(1084830) OTHER INFORMATION: n equals a, t, c	MAME/KEY: misc_feature LOCATION: (1096846)(1096846) OTHER INFORMATION: n equals a, t, c	NAME/KEY: misc feature LOCATION: (1119881)(1119881) OTHER INFORMATION: n equals a, t, c	NAME/KEY: misc_feature LOCATION: (1130881)(1130881) OTHER INFORMATION: n equals a, t, c	NAME/KEY: misc_feature LOCATION: (1310988)(1310988) OCHER INFORMATION: n equals a, t, c FEATURE:	NAME/KEY: misc feature LOCATION: (1313224)(1313224) COCHER INFORMATION: n equals a, t, c FEATURE: NAME/KEY: misc feature LOCATION: (13459473)(1349473)	2.6e-29 392.50 40.05%		US-09-515-363C-2 (1-1025) x US-09-692-570-1  Qy		1658898 161611ITAICGACAGGITIAG 346 HisleuAspLysLysLysLysAlaS 1658905 ATTTAACAAAAAG				426 AsnGlyGluAspAlaGlyValG	445 CysHisHisThrAsnLysGluAlaValTyrA

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978 AGTGGGCTTTATGAAAGACTGCTGATGGAATTAGAAGAAGCACTTAATTTATCAATGAT 1037
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TCAGACTGTCGTGCCGTATTGGTAGTTCTGGGACCCTGGTGTGCAGATAAAGTAGCTGGA 1157
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                                                                                         LeuProThrGlySerGlyLysThrArgValAla---ValTyrIleAlaLysAsp----- 345
                                                                                                                                                                                                                                                                                                                                                                                                                     TIGAAIGITITIGAAAAT------GGTACTTACTTATCACTGTCAGACATT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuileilelehapGluCysHisHisThrAsnLysGluAlaValTyrAsnAsnIle 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    924 TATACTTCTCAGCCATGTGAG-----ATTGTGGTGGATTGTGGACCATTTACTGACAGA 977
                                ArgProTyrGlmMetGluValAlaGlnProAlaLeuGluGlyLyBAsnIleIleIleCyg 328
                                                                                                           TCTGCAAACCAGGTTGCTCAACAAGTGTCAGCTGTCAGAACTCATTCAGATCTCAAG--- 548
                                                                                                                                                                                                                                                                                                                                   -----ProGluValValLysSerCysAspilellelleSerThrAlaGlnIleLeu 417
                                                                                                                                                                                                                                                                                                                                                                                             GludsnSerLeuLeudsnLeuGludsnGlyGludspAlaGlyValGlnLeuSerAspPhe 437
                                                                                                                                                    HistonAspLysLysLysLysAlaSerGluProGlyLys---ValIleValLeuValAsn 364
                                                                                                                                                                                                            Lysval---LeuLeuValGluGlnLeuPheArgLysGluPheGlnProPheLeuLysLys 383
                                                                                                                                                                                                                                                                                                    ------GTTGGGGAATACTCAAACCTAGAAGTAAATGCATCTTGGACAAAGAG 596
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                                                           AGAAAATATCAGGTTGAACTGCTTGAAGCAGCTCTGGAT---CATAATACCATCGTCTGT
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                 1660171 GCTTTATACAAAGAAGGGAGATGATGATTATTAAAAAATATGTGTTATTTGCTAAAT 1660230
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                                                         808 GlyLeuValThrAsnGluIleAlaMetValGlnAlaArgGlyArgAlaArgAlaAspGlu 827
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AlaThrThrValAlaGluGluGlyLeuAspileLysGluCysAsnIleValIleArgTyr 807
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Patent No. 644466
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TILLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
FILE REFERENCE: RTS-02.7
CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 3
LENGTH: 7037
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Matches:
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
Query Match:
DB:
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Qy   938 LeuTyrIleValArgGluAenLyeAla	Qy         965 yGlnalaTrpGlyThrMetMetValHis	RESULT 9 US-09-408-020-65 ; Sequence 65, Application US/09408020 ; Patent No. 6632937 ; GENERAL INFORMATION: ; APPLICANT: Swanson, Rohald V. ; APPLICANT: Feldman, Robert A. ; APPLICANT: Schleper, Christa	; FILE REFERENCE: DCORP.002A ; CURRENT APPLICATION NUMBER: US/09/408,020 ; CURRENT PILING DATE: 1999-09-29 ; PRIOR PPLICATION NUMBER: 60/102,294 ; PRIOR APPLICATION NUMBER: 60/102,294 ; PRIOR APPLICATION NUMBER: 60/102,294 ; PRIOR APPLICATION NUMBER: 60/103,294 ; RIUNGER OF SEQ ID NOS: 123 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 65	LENGTH: 1512 	Alignment Scores: 7.43e-23 Length: 1512 Pred. No.: 289.50 Matches: 137 Score: 289.50 Matches: 137 Percent Similarity: 23.40% Conservative: 88 Best Local Similarity: 23.99% Mismatches: 188 Query Match: 5.45% Indels: 23 DB:	US-09-515-363C-2 (1-1025) x US-09-408-020-65 (1-1512)  Qy	Qy         322 GlyLygAbnIleIleIleCygleuProThrGlySerGlyLygThrArgValAlaValTyr 341           bb         94GAAAACTGCATAGTGGTGCTGCCTACCGGCACTGGCCCTGGCCCTGGCCTTGCAG 150           Qy         342 IleAlaLygAspHisLeuAspLygLygLygLygLygAlaSerGluProGlyLygValIleVal 361           i::
AspThr:::: GAAATC TyrAsn AATAAT ASPASP		GluAsnProGluTyrGluAsnGluLysLeuThrLysLeuArgAsnThrIleMetGluGln 7		SetSetUprallPheapperrometThrGinAsholuGlnLysGluVallleSetLysPheArg 779   1671 GAAGCAGATTCAGAAAACAGGAAGAGGTACTTAGGAAATTTCGA 1715   780 ThrGlyLysIleAsnLeuLeuLeuLleAlaThrThrValaGluGluGluGlyLeuspIleLys 799   1716 GCACATGAGACCTGCTTATTGCAACAAGTATTGTAGAAGAGGTGTTGATATACCA 1775	800 GlucysAsnileValileArgTyrGlyLeuValThrAsnGluileAlaMetValGlnAla 819 :::      ::    ::    ::    ::     :	840 ValileGluHisGluThrValAsnAspPheArgGluLysMetMetTyrLysAlaile 858 ::: ::: ::: 1881GATACAGACAAAATAAAAGTTTTGAAGAAGACCTTAAAACCTACAAAGCTATT 1934 859 HisCysValGlnAsnMetLysProGluGluTyrAlaHisLysIleLeuGluLeuGlnMet 878	1934

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Sequence 33, Application US/09408020
Sequence 33, Application US/09408020
Sequence 33, Application US/09408020
Sequence 34, Sediaman, Robert A.
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/9408,020
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
SPRIOR FILING DATE: 1998-09-29
SPRIOR FILING DATE: 1998-09-29
SOFTWARE: FASEQ for Windows Version 3.0
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Indels:
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DB:
CDS
(28065).
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1078 CTCATA-----CACTCAAGACTCAAGGCGGCCGGGATAAACTCGGGC 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 ThrGluGluSerAlaArgGly-----IlellePheThrLysThrArgGlnSerAlaTyr 732
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       676 GCCCTCGAC---GAGAGGTATTCCTCCCTCAAGAGGTGCGGGTACGATCTTGGCTCGAAC 732
                                                                                                                                                                                                                                                                                                              655 AspGlyAspGluAspGluAspAspLeuLysLysProLeuLysLeuAspGluThrAspArg 674
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Batent No. 6612937

GENERAL INFORMATION:
APPLICANT: Swalson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT PILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ 1D NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1024 -----CGCGGGGCCCGGGGAAAGGCGCTGGTCTTTACGAGCTATCGTGATTCTGTCGAC
                                                                                                                             LysGluValIleSerLysPheArgThrGlyLysIleAsnLeuLeuIleAlaThrThrVal
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                                      577 ProTyrGluGlnTrpAlaIleGlnMetGluLysLysAlaAlaLysLysGlyAgnArgLys
                                                                        733 AGGTCGCTCTCGGCGCTGCTCCGGCTG---CGCATGGTGGTGCTTGGCGGCACAGGCGC
                                                                                                        GluargvalCysAlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnIleAsnAspThr
                                                                                                                                                                         617 IleArgMetIleAspAlaTyr----ThrHisLeuGluThrPheTyrAsnGluGluLys
                                                                                                                                                                                                         832 CTAAACATATTCGAGGCGCACGGGTCACGCCCTTTCTAAAGTTCTGCGAGAGGACCTCC
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US-09-408-020-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 GGCCTGGTCATATTCGACGCGCCCCACAGGCGGTGGGCGACTATGCCTATTCTTCCATA 450
                                                                                                                                                                                                                                                                                                                                                                                                                 94 ----GAGAACTGTATCGTGGTGCTCCCGACGGCCTCGGCAAGACTGCCGTCGCCCTCCCAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTAAAC------CAGCACCGCCAGTTCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLysTrpTyrArgValIleGlyLeuSerGlyAspThrGlnLeu-----LysIleSer 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 GluAsnSerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPhe 437
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GTAGGGGATAACTCCAGGATGGTGGCATGACTGCGACGCTT------CCCAGC 507
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                                                                                                                                                                                                                                                                                                                            GluPro---GluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeuGlu 321
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                                                                                                                                                                                                                                                                                                                                                 342 IleAlaLysAspHisLeuAspLysLysLysAlaSerGluProGlyLysVallleVal
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133
94
207
114
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                   TYPE: DNA ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                      3.2e-22
284.00
41.42%
24.27%
5.35%
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Best Local Similarity:
Query Match:
DB:
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                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-09-408-020-33
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SEQ ID NO 33
LENGTH: 1509
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1227

SOFTWARE: FastSEQ for Windows Version 3.0 SRO TD NO 2	ò	400 PheProGluValVallysSerCysAspilellelleSerThrAlaGlnIleLeu 417
LA IL NO 2 LA IL NO 2 MUNDTH: 42432	qq	34847 ATTCCCGGCGCAAAAAGCGGTGGGGAGGCAGCGTGATCTGCGCCCACACGCCGAGATAGCA 34906
1res: UNA PRAMISM: Cenarchaeum symbiosum BERMITHER:	ò	418 GluAsnSerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlýValGlnLeuSerAspPhe 437
FEATURE: TACATION: (3) (10421)	qa	34907 AGAAATGATATA
· · · · · ·	à	438 SerLeullellelleleAspGluCysHisHisThrAsnLysGluAlaValTyrAsnAsnIle 457
	qa	34949 ggccidgicalaricakdadgccdadaggcggraggggagrargcciaricticcara 35008
NAME/KEY: CDS LOCATION: (11478)(13046)	ð í	HisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLysGluAsnLysPro
: CDS	g (	3CGCGG
LOCATION: (13046)(14620) MANAGATON: (13046)(14620)	ð f	478 VALIIEPTOLEUPTOGINIIELEUULYLEUNINTALASETPTOGIYVAIGLYVALALNII 497 316118 GTBGGGGGBTBARTTCCAGGARGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	3 8	LysglnAlaLysAlagluGluHisIleLeuLysLeuCysAlaAsnLeuAspAlaPheThr
NAME/KEY: CDS LOCATION: (24913)(25728)	. A	GAGAGGAAAGGCAGACGAGACGAGACGAGAGGAGCCCTGCTCCCAGGAGG
FEATURE: NAME/KEY: CDS LOCATION: (26504)(26881)	٥٧	
CDS	q	
	<i>8</i> €	538 LysPheAlaIleAlaAspAlaThrArgGluAspProPheLysGluLysLeuLeuGluIle 557 :::::       :::::       ::::: 35133
	ò	
NAME/KEY: CDS LCCATION: (37002)(37403)	qq	35234 GCCCTCGACGAGAGGTATTCCTCCCTCAAGAGGTGCGGGTACGATCTTGGCTCGAAC 35290
FEATURE: NAME/KEY: CDS LOCATION: (37404)(38282)	λō	ProTyrGluGlnTrpAlaileGlnMetGluLysLysAlaAlaLysLysGlyAsnArgLys
: CDS	음 &	
LOCATION: (39454)(405/2) S-09-408-020-2	<u></u>	357 GIUAIGVAILVEBAIAGIUAIGEBUAIGHAYSIYAASIGALAHAAGAAAAAGAAAAAAGAAGAAGAAGAAGAAGAAGAAGA
1.24e-19 Length: 284.00 Matches:	ð í	IleargMetIleAspAlaT
.Larity: 41.42% Conservative: :imilarity: 24.27% Mismatches:	g G	35390 CIARACAIAII CGAGGCGCACGGGGI CACGCCCIII CIARAGII CIGCGAGAGAGCACCIIC
4. 3.3. 4.	<i>₹</i> 6	635 ApplystysPheAlaVallleGluAspAspSsrAspGluGlyGlyAspAspGluTyrCys 654
US-09-515-363C-2 (1-1025) x US-09-408-020-2 (1-42432)	8	sLysProLeuLysLeuAspGluThrAspArg
GluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProAlaLeuGlu	QQ	35477CTGTTCGAACAGGACCGG 35494
GAGCCCGGTGCCGTCGAGAGGCGCGACTACCAGGTGGGCCTGGCGGAAACAGGCCCATACGG	ò	675 PheLeuMetThrLeuPhePheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnPro 694
322 GIYLYBABRILELIELYBLERIFOTHRGIYSEKGIYLYBHIRANGYALAIAVALIYY 341  -:-   -	qq	
11eAlaLy8AspHisLeuAspLysLysLysLaSerGluProGlyLysVallleVal	ò 5	695 GluTyrGluAanGluLyaLeuThrLyaLeuArgAanThrIleMetGluGluGluTyrThrArg 714  11
34709 GIGATCGCCCACTATCTCGACGAGGCCGCGGGGGCGCTTCCTTGCCCCTACAAGGGTC 34768	8 8	
LeuvaldenLysValLeuLeuValGluGlnLeuPheArgLysGluPheGlnProPheLeu 381	ු සි	
CTGGTAAACCAGCACCGCCAGTTCCTG	ò	733 AlaLeuSerGlnTrplleThrGluAsnGluLysPheAlaGluValGlyValLysAlaHis 752
382 LysLysTrpTyrArgVall1eGlyLeuGerGlyAspThrGlnLeuLysIleSer 399 3426 Coc	qa	35636 CTCATA
77474777777777777777777777777777777777	λο —	753 HisLeulleGlyAlaGlyHisSerSerGluPheLysProMetThrGlnAsnGluGln 771

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947 LeuGlnLysLysCysAlaAspTyrGlnIleAsnGlyGluIleIleCysLysCysGlyGln
                                                                                 1 CTGCAAAGAAGTGTGCCGACTATAA-ATAAATGTGAAATCATCTGCAAATGTGGCCAG
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Matches:
Conservative:
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227.50
75.36%
72.46%
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Best Local Similarity:
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US-09-221-268D-11
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  792 AlaGluGluGlyLeuAspileLysGluCysAsnIleValileArgTyrGlyLeuValThr 811
                                                                                                                                                                                                                                                                                    812 AsnGluileAlaMetValGlnAlaArgGlyArg---AlaArgAlaAspGluSerThrTyr 830
                                                                           LysGluVallleSerLysPheArgThrGlyLysIleAsnLeuLeuIleAlaThrThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08143576
Patent No. 5643761
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
APPLICANT: Jiang, Hongping
TITLE OF INVENTION: METHOD FOR GENERATING A SUBSTRACTED
TITLE OF INVENTION: CDNA LIBRARY AND USES OF THE GENERATED LIBRARY NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,576
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43563/JPW/AKC
TELEFRANCE/LOCKET NUMBER: 43563/JPW/AKC
TELEFRANCE/LOCKET NUMBER: 22,678
TELEFRANCE/LOCKET NUMBER: 22,678
TELEFRANCE/LOCKET NUMBER: 22,678
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TELEFRANCE/LOCKET NUMBER: 212,64-0525
TELEFRANCE/LOCKET NUMBER: 212,64
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Matches:
Conservative:
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35678 ATCCTGATAGGAAAGGCGGGAGA-
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Sequence 11, Application US/09221268D

Patent No. 6720408

Barent No. 6720408

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH SPECIFICALLY HYBRIDIZE WITH
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING MDA-7 AND PHARMACEUTICAL COMPOSI
FILE REFERENCE: A34534-A-A (070050.1637)
CURRENT APPLICATION NUMBER: US/09/221,268D
CURRENT FILING DATE: 1994-09-30
PRIOR PILING DATE: 1994-09-30
PRIOR APPLICATION NUMBER: 08/316,537
PRIOR FILING DATE: 1994-09-30
PRIOR PRIOR APPLICATION NUMBER: 08/143,576
PRIOR PILING DATE: 1993-10-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 193
                                                                                                                                                                                          987 PhevalvalvalPheLysAsnAsnSerThrLysLysClnTyrLysLysTrpvalGluLeu 1006
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                                                              967 AlaTrpGlyThrMetMetValHisLysGlyLeuAspLeuProCysLeuLysIleArgAsn
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1489 GAAATTGTAGCTAAACACCLTGGAAACTGAAGAGGAACTTAAAGTTGCTCATTGTTGCCTG 4548
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CTACAGAGGCTGCAAGAAGTTCTTCAATCTGAAAGTGACCAGCTCAAAGAAAACATAAAA 4488
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TTCAAACCCAAAGATTCAGCACTACTAAGGATAGAAATAGAAATGCTCGGATTGTCC--- 4371
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8895 CAGGACTTAGAAAAATCCCATACCAAATTACAAGAAGAGATCCCAGTGCTTCATGAGGAA 3954
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    193 LeuvalGlnGluLeuThrGlySerAspCysSerGluSerAsnAlaGluIleGluAsnLeu 212
                                                                                                                               222 GluGlnLeuLeuSerThrThrValGlnProAsnLeuGluLysGluValTrpGlyMetGlu 241
                                                                                                                                                                                             242 AsnAsnSerSerGluSerSerPheAlaAspSerSerValValSerGluSerAspThrSer 261
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                                                                                                                                                                                                                                                                                                                      282 SerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAlaSer 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3418 AAGAAAGAAGGAGGCTTTCTAGGACCTGTGACAGACTGGCAGAAGTTGAAGAAAAAACTA 3477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3718 AAGTCATTTGAAACAGAGAGAGCCACCTTAGAGGATATATAAGAGAAATTGAAGCTÄĊÄ 3777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrreuvalAspLysLeuLeuValArgAspVal-----LeuAspLysCysMetGluGlu 141,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuAsnLeuLeuGlnPro 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluProvalLeuAspTyrLeuThrPheLeuProAlaGluValLysGluGlnIleGlnArg 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GluAsnPheArgTyrLeuIleSerCysPheArgAlaArgValLysMetTyrIleGlnVal
APPLICANT: Sakowicz, Roman
APPLICANT: Vaisberg, Eugeni
APPLICANT: Waisberg, Eugeni
APPLICANT: Wood, Kenneth
TYLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: Cytopo36
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR PELLING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 8257
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209
185
421
307
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Mismatches:
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Matches:
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217.50
35.12%
18.63%
4.10%
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Best Local Similarity:
                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                   ; ORGANISM: Hum:
US-09-595-684B-30
                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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Perfect score: Sequence: Scoring table:

Searched:

OM protein

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Sequence 771, App Sequence 2072, App Sequence 2072, App Sequence 2033, App Sequence 2133, App Sequence 21563, A Sequence 21563, A Sequence 2101, App Sequence 2101, App Sequence 25, App Sequence 25, App Sequence 25, App Sequence 27, App Sequence 17, App Sequence 27, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 27, App Sequence 27, App Sequence 521, App Sequence 521, App Sequence 521, App Sequence 5208, A Sequence 5208, A Sequence 5208, A Sequence 5208, A Sequence 5208, A
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                                                                                                                                            Sequence 405, Applisequence 8, Applisequence 1042, A Sequence 1, Applisequence 1, Applisequence 6057, Applisequence 61, Applisequence 48, Applisequence 48, Applisequence 48, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, Applisequence 61, 
                                 Description
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APPLICANT: Kang, Dong-Chul
APPLICANT: Kang, Dong-Chul
APPLICANT: Gapalkrishnam, Rahul V.
TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
CURRENT APPLICATION NUMBER: US/10/055,475
CURRENT FILING DATE: 2002-01-22
FRIOR APPLICATION NUMBER: 09/515,363
FRIOR FILING DATE: 2000-02-29
FRIOR PILING DATE: 2000-02-29
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US-10-437-963-30018
US-10-369-493-45047
US-09-938-842A-887
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US-10-828-924-70
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US-09-864-761-31791
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Query
Match Length
                                                                                                                                                                                                                                                                                                                                                   US-10-055-475-1
                                                                                  Result
No.
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-DB=bublished Applications NA -QFMT=fastap -SUFFIX=rnpb -MIRNATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGARPOP=6 -FGAPEXT=7 -YGARPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                            - nucleic search, using frame_plus_p2n model
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                            Sequence 1, Application US/10228897
; Publication No. USG030092043A1
; Publication No. USG030092043A1
; CENERAL INFORMATION:
    APPLICANT: Fasher, Paul B.
    APPLICANT: Kang, Dong-Chul B.
    APPLICANT: Kang, Dong-Chul B.
    APPLICANT: Gopalkrishnan, Rahul V.
    APPLICANT: Gopalkrishnan, Rahul V.
    APPLICANT: Gopalkrishnan, Rahul V.
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    APPLICANT: Gopalkrishnan, Rahul V.
    APPLICANT: Gopalkrishnan, Rahul V.
    APPLICANT: Gopalkrishnan, Rahul V.
    APPLICANTON: GENE-5 AND PROMOTER AND USES THEREOF
    FILE REFERENCE: A34614-A-FCT-USA (070050.2121)
    CURRENT FILING DATE: 2002-08-26
    PRIOR PILING DATE: 2000-02-29
    PRIOR PILING DATE: 2000-02-29
    NUMBER: O9/515,363
    PRIOR PILING DATE: 2000-02-29
    NUMBER: PastSEQ for Windows Version 4.0
    SEQ ID NO 1
    LENGTH: 3365
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TYPE: DNA
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
FILE SEPERANCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.2
SSOFTWARE: PatentIn version 3.2
SSOFTWARE: 23.60
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Publication No: US20040171823A1
GENERAL INFORMATION:
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Best Local Similarity:
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                              rgraacarrgrrarcgrrarggrcrcgrcaccaargaaaragccarggrccaggcccgr
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; Bublication No. US2030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Application Now-Chul
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL
; FILE REPRENCE: A4614-A-PCT-USA-A (07050-1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT APPLICATION NUMBER: US/10/055,475
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PSECSE OF WINGOWS Version 4.0
; SECTION NO
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CORGANISM: homo sapiens
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Length: Matches: Conservative: Mismatches: Indels: Gaps:	MetSerAsnG.yTyrsserThrAspGlubsnPhehrgTyrLeulleSerCygPheA	GluValLysGluGlnIleGlnArgThrValAlaThrSerGlyAsnMetGlnAlaV 	LeuLeuLeuSerThrLeuGluLysGlyValTrpHisLeuGlyTrpThrArgGluP	GAGGCCCTCCGGAGAACCGGCAGCCTCTGGCCGCCCGCTACATGAACCCTGAGC ASpLeuProSerProSerPheGluAsnAlaHisAspGluTyrLeuGlnLeuLeuA 	LeuGInProThrLeuValAspLysLeuLeuValArgAspValLeuAspLysCysM 	GluGluLeuLeuThrIleGluAspArgAsnArgIleAlaAlaAlaGluAsnAsnG 	GluSerGlyValargGluLeuLysArglleValGlnLysGluAsnTrpPheS 	PheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeuValGlnGluLeuThrG 	AspCysSerGluSerAsnAlaGlu1leGluAsnLeuSerGlnValAspGlyProG 	GluGluGlnLeuLeuSerThrThrValGlnProAsnLeuGluLysGluValTrpG 	erPheAlaAspSerS 	SerleualagluglySerValSerCysLeuaspgluserLeuglyHisasnSerA 	GlySerAspSerGlyThrMetGlySerAspSerAspGluGluAsnValAlaAlaA 	SerProGluProGluLeuGlnLeuArgProTyrGlnMetGluValAlaGlnProA
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Alignment Scores: Pred. No.: Scoret Scoret Similarity: Percent Similarity: Query Match: DB: US-09-515-363C-2 (1	1 MetS           169 ATGT 21 ArgV 22 ArgV			409 GAGG 101 ASPL      469 GACT	121 LeuG       529 CTTC	141 GluG      589 GAGG	161 Glus      	181 PheL      709 TTTC	201 AspC       769 GATT	221 GluG      829 GAAG	241 GluA      889 GAGA	261 SerL      949 AGTT	281 GlySerAs          1009 GGCAGTGA	

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GluSerGlyValArgGluLeuLeuLysArgIleValGlnLysGluAsnTrpPheSerAla
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                                                            AND METHODS
PREVENTION,
JUS-10-198-846-13042

Sequence 13042, Application US/10198846

Publication No. US2030099974A1

GENERAL INFORMATION:

APPLICANT: Lilie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

TITLE OF INVENTION: POR IDENTIFICATIONS, KITS, AND

TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PRENT

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2001-07-18
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13042
LENGTH: 3928
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NAMME/KEY: misc_feature

LOCATION: 1, 3925, 3926, 3927, 3928

COTHER INFORMATION: n = A,T,C or G

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ORGANISM: Homo sapiens
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US-10-723-860-5057

Sequence 5057, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: April.
APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

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TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT APPLICATION NUMBER: 60/429,739

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOC ID NO 5057

LENTH: 3668
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AspGluTyrCysAspGlyAspGluAspGlu 660 ABIGIUGIULYBASDLYBLYBPHEAIAVAI 640 JAIAGIUABNPrOGIUTYrGIUABNGIULYB 700 1848 1368 GlualavalTyrasnasnilemetarghis 460 AlaAsnLeuAspAlaPheThrIleLysThr 520 Ginilegingluprocystystystyspheala 540 SerAapPheGlyThrGlnProTyrGluGln 580 260 400 SerGlyAspThrGlnLeuLysIleSerPhe

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Matches:
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APPLICANT: OTSUKA, KAORU
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APPLICANT: TRIE, RYOTARO
APPLICANT: SEKI, NAGHIKO
APPLICANT: SCHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGHARI, KENJI
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APPLICANTON NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
NUMBER: PREGION NUMBER: JP 2001-328381
NUMBER: OF SEQ ID NOS: 3381
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LENGTH: 1776
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Best Local Similarity:
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                                                                                                                                  SerGluPheLysProMetThrGlnAsnGluGlnLysGluValIleSerLysPheArgThr
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                                                                741 AsnGluLysPheAlaGluValGlyValLysAlaHisHisLeuIleGlyAlaGlyHisSer
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721 GlyileilePheThrLysThrArgGlnSerAlaTyrAlaLeuSerGlnTrpIleThrGlu
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Sequence 828, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: GUGIYAMA, TOMOYASU
APPLICANT: WARAMATSU, AI
APPLICANT: WARAMATSU, AI
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Matches:
Conservative:
Mismatches:
Indels:
                           n = A, T, C or
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2442.00
99.38%
98.96%
45.98%
                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;

LOCATION: 927

CTHER INFORMATION: n =

US-10-275-822A-10
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Best Local Similarity:
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                                                                                                                             ThrGluGluSerAlaArgGlyIleIlePheThrLysThrArgGlnSerAlaTyrAlaLeu
                                                                                                                                       SerGInTrp1leThrGluAsnGluLysPheAlaGluValGlyValLysAlaHisHisLeu
                                                                                                                                                                        ATTGGAGCTGGACACAGCAGTGAGTTCAAACCCATGACACAGAATGAACAAAAAGAAGTC
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                                                                                             GluTyrGluAsnGluLysLeuThrLysLeuArgAsnThrIleMetGluGlnTyrThrArg
                                                                                                        GAATATGAAAATGAAAAGCTGACCAAATTAAGAAATACCATAATGGAGGAATATATGTAGA
   PheLeuMetThrLeuPhePheGluAsnAsnLysMetLeuLysArgLeuAlaGluAsnPro
                                                                     AspGlyAspGluAspGluAspAspLeuLysLysProLeuLysLeuAspGluThrAspArg
                                            GATGGTGATGAAGATGATGATTTAAAGAAACCTTTGAAACTGGATGAACAGATAGA
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RESULT 10

US-10-275-822A-10

US-10-275-822A-10

Sequence 10, Application US/10275822A

Publication No. US20040086500A1

GENERAL INFORMATION:
APPLICANT: BATA, Georges

APPLICANT: Cocude, Cecile

APPLICANT: Cocude, Cecile

APPLICANT: Cocude, Cecile

APPLICANTION: Hall 6 Polypeptide and its Fragments and Polynucleotides Encoding

TITLE OF INVENTION: Said Polypeptides and Therapeutic Uses

FILE REPERENCE: 017753-170

CURRENT APPLICATION NUMBER: VOS/10/275,822A

CURRENT APPLICATION NUMBER: PCT/FR01/01441

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-11

STORYMARE: FROM OF 056 11

NUMBER OF SEQ ID NOS: 56

SEQ ID NO 10

LENGTH: 1443 273 213 121 253 241 301 361 421 61 LeuGlyHisAsnSerAsnMetGlySerAspSerGlyThrMetGlySerAspSerAspGlu GluLysGluValTrpGlyMetGluAsnAsnSerSerGluSerSerPheAlaAspSerSer 194 ValGlnGluLeuThrGlySerAspCysSerGluSerAsnAlaGluIleGluAsnLeuSer LysGluAsnTrpPheSerAlaPheLeuAsnValLeuArgGlnThrGlyAsnAsnGluLeu

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Matches:
Conservative:
Mismatches:
Indels:
                                                                       NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-515-363C-2 (1-1025) x US-10-641-643-48 (1-1392)
                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Wind
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-ANG-2003
CLASSIFICATION: <UNKNOWN>
          TITLE OF INVENTION: COMPOSITION FOR GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: AUNKNOWN>
ATTORNEY/AGBNT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-0001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO: 48
   APPLICANT: Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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IMMEDIATE SOURCE:
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Best Local Similarity:
Query Match:
DB:
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GluValAlaGlnProAlaLeuGluGlyLysAsnIleIleIleCysLeuProThrGlySer
                 GAAGTTGCCCAGCCAGCCTTGGAAGGAAAATATCATCATCTGCCTCCCTACAGGGAAGT
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GENERAL INFORMATION:

APPLICANT: Bahr, Georges

APPLICANT: Cocude, Cecile

APPLICANT: Capron, Andre

TITLE OF INVENTION: RH116 Polypeptide and its Fragments and Polymucleotides Encoding

TITLE OF INVENTION: RH116 Polypeptides and Therapeutic Uses

TITLE OF INVENTION: Said Polypeptides and Therapeutic Uses

FILE REFERENCE: 017753-170

CURRENT APPLICATION NUMBER: US/10/275,822A

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: FR 00/06,030

PRIOR FILING DATE: 2000-05-11

PRIOR FILING DATE: 2000-05-11

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7
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NAME/KEY: misc_feature

LOCATION: 1261

OTHER INFORMATION: n = A,

US-10-275-8228-7
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                      LENGTH: 1284
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                             TTAAGAAATACCATAATGGAGCAATATACTAGGACTGAGGAATCAGGCACGAGGAATAATC
                                                          PheThrLysThrArgGlnSerAlaTyrAlaLeuSerGlnTrpIleThrGluAsnGluLys
                                                                                 TTTACAAAAACACGACAGAGTGCATATGCGCTTTCCCCAGTGGATTACTGAAAATGAAAAA
              LeuArgAsnThrIleMetGluGlnTyrThrArgThrGluGluSerAlaArgGlyIleIle
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5-10-275-822A-7
Sequence 7, Application US/10275822A
Publication No. US20040086500A1
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846 ValASDAGGACCTACCTCGGTTGCTCACAGTGGTTCAGGAGTTATCGAACGTGAGACACAGGACTACGAGCACACGTGACACAGGAGTTATCGAACGTGGTTGCTCACAGGAGTTTATCGAACGTTGCTTCAAATTGATTCAAAATTGATTTCCGAGAGAAGAATTTCCGAAGAAGTTTTCGAAGATTTTCGAAGAATTTCCGAAGAATTTCCGAAGAATTTCCGAAGAATTTCCGAAGAATTTCCAAATTGATTTTCGAAGAATTTCCGAAGAATTTCCAAATTGATTTTCGAAGAATTTCCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTTCCAAGAATTACAAGAATTACAAGAATTACAAGAATTACAAGAATTACAAGAATAACCAAGAAAACTTCCAAGAAATATTCCCAAGCAATTACAAGAATAACCCATCAATAAATA	Sequence 71, Application US/10302172

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AsnArgLeuLysLysGluAsnLysProVallleProLeuProGln1leLeuGlyLeuThr 488
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFRENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; UWRRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 2072
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US-10-108-260A-2072
                                              US-10-108-260A-2072
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                     AspPheArgGluLysMetMetTyrLysAlaIleHisCysValGlnAsnMetLysProGlu 867
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; Sequence 1472, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INPORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Work to Ver, Laura
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van 'de Vijver, Marc
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Van 'Sernerale, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of E
; FILE REPRENCE: 3010-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-06-14
; WUMBER OF SEQ ID NOS: 2699
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DATABASE ENTRY DATE: 2001-06-18
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Best Local Similarity:
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2342 GGCAGAGGAAGAGGAAGGGAAGTGCTTCCTTCTGACT---AGTAATGCTGGTGTA 2398
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2621 GACGTAAGAGGATGAATGCCATTACACTGTGCTTGGAGATGCTTTTAAGGAATGC 2680
                     2516 -----GAAAAATTCATCAGAGATAGTCAAGAAAAACCAAAAACCTGTCCCTGATAAGGAA 2569
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2162 CAGAACACAGGAATGACCCTCCCGGCACAGAAGTGTATATTGGATGCATTCAAAGCCAGT 2221
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|681 TTTGTGAGTAGACCACTCCCAAG---CCAAAGCAGTTTTCAAGTTTTGAAAAAAAGCA 2737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                976 GlyLeuAspLeuProCysLeuLysIleArgAsnPheValValValPheLysAsnAsnSer 995
684 AsnLysMetLeuLysArgLeuAlaGluAsnProGluTyrGluAsnGluLysLeuThrLys 703
                                                             LeuArgAsnThrileMetGluGlnTyrThrArgThrGluGluSerAlaArgGlyIleile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        939 TyrileValArgGluAsnLysAlaLeuGlnLysLysCysAlaAspTyrGlnIleAsnGly
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Search completed: January 28, 2005, 05:01:05 Job time : 1273 secs This Page Blank (uspło)

us-09-515-363c-2.rpr

10

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 26, 2005, 19:36:55 ; Search time 49 Seconds (without alignments) 2012.698 Million cell updates/sec Run on:

US-09-515-363C-2 5311 1 MSNGYSTDENFRYLISCFRA......LPITFPNLDYSECCLFSDED 1025 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dР			SUMMALES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
ч	9	12.9	1037	2	T32534	hypothetical prote
7	654	12.3	811	~	T30968	
ო	642.5	12.1	926	~	A88708	protein C01B10.1 [
4	516	9.7	398	~	T46312	hypothetical prote
ß	499	9.4	1134	~	T20332	
9	453	8.5	752	~	D75219	₽
7	441.5	8.3	650	7	D71203	probable ATP-depen
æ	417	7.9	741	Н	A69432	ATP-dependent RNA
σ	402.5	7.6	1374	7	S62524	probable RNA helic
10	392.5	7.4	784	~	H64487	eIF-4A family prob
11	350	9.9	1822	~	S44849	K12H4.8 protein -
12	342	6.4	738	Н	E69055	ATP-dependent RNA
13	313.5	5.9	784	7	D84386	ATP-dependent RNA
14	303.5	5.7	993	~	S48436	probable RNA helic
15	284	5.3	502	7	T31323	ATP-dependent RNA
16	278.5		839	~	T39190	probable ATP-depen
17	223	4.2	557	7	G69958	SNF2 helicase homo
18	218	4.1	1979	7	C71622	hypothetical prote
19	217.5	4.7	2663	-	S28261	×
20	214.5	4.0	1790	~	S67593	transport protein
21	209.5			7	C71156	_
22	205	3.9		7	B75006	DNA repair protein
23	205			~	D72308	conserved hypothet
24	204.5	•	N	N	S50675	
25	204	٠	_	~	T18372	repeat organellar
56	201.5	•	-	~	T38420	probable DNA helic
27	198.5	3.7	2253	~	T30336	nuclear/mitotic ap
28	197.5		16	N	G97236	
53	195	3.7	1531	7	T48946	hypothetical prote

giantin - human	restriction-modifi	hypothetical prote	hypothetical prote	exinuclease ABC su	myosin heavy chain	myosin II heavy ch	giantin - human	DNA helicase relat	restriction modifi	hypothetical prote	CGI protein - huma	HadRi protein - My	kinectin 1 - human	ATP-dependent RNA	hypothetical prote
A56539	E90596	T26101	E72734	G89848	A36014	S61477	152300	B75135	H90565	E71100	153799	549394	S32763	F69543	T00637
-	7	~	~	~	-	~	7	~	7	~	7	~	~	N	7
259	986	1256	1039	663	2017	2057	3225	715	986	718	1300	986	1356	943	1922
m															
3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
195 3.7 33	194.5 3.7	194.5 3.7	194 3.7	193.5 3.6	193.5 3.6	193.5 3.6	193.5 3.6	193 3.6	193 3.6	192.5 3.6	192.5 3.6	192 3.6	192 3.6	191.5 3.6	191 3.6

## ALIGNMENTS

-	RESULT 1 T32534 hypothetical proteir C;Species: Caenorhab C;Date: 29-Oct-1999 C;Accession: T32534 R;Wohldmann, P; Mun submitted to the EMI A;Description: The E	RESULT 1 T32534 Typothetical protein F15B10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T32534 R;Wohldens T92534 R;Wohldens to the EMBL Data Library, December 1997 Submitted to the EMBL Data Library, December 1997 B, Paesrathoin: The sequence of C. elegans cosmid F15B10.
· · ·	A, Status: preliminary; t A, Status: preliminary; t A, Molecule type: DNA A, Residues: 1-1037 «WOH> A, Experimental source: 9 C, Generics: C, Generics:	A;Accession: 132534 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Acleuse: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Acces-references: UNIPROT:044165; EMBL:AF036696; PIDN:AAB88350.1; GSPDB:GN00022; CESP A;Experimental source: strain Bristol N2; clone F15B10 C;Genetics: A;Gene: CESP:F15B10.2
	A; may position: 4, Introns: 30/3; Query Match Best Local Simi Matches 251;	A; Introns: 30/3; 89/1; 111/2; 218/1; 258/2; 288/1; 343/3; 370/3; 400/2; 443/1; 520/1; 5 Query Match 1037; 400/2; 443/1; 520/1; 5 Query Match 1037; 12:9%; Score 687; DB 2; Length 1037; Best Local Similarity 25.0%; Pred. No. 2. 9e-27; Matches 251; Conservative 169; Mismatches 408; Indels 174; Gaps 35;
	Oy 10:	101 DLPSPSFENAHDEYLQLLNLLQPTLVDKLLVRDVLDKCMEEE 142 
	Oy 14:	143 LLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSAFLNVLRQTGNNELVQ 195 
	Oy 190 Db 18	196 ELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGMENN 243   :-
-1.	Qy 24-	244 SSESSFADSSVVSESDTSLAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENV 296 1
	Qy 29°	297 AARASPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEP 356   ::
<u>.</u>	Oy 35'	357 GKVIVLV-NKVLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQ 415
	Qy 41( Db 39)	416 ILENSLLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNR 470 

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protein COIBIO.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88708
B;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_eleans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Noteule: Uppe: DNA
A;Residues: 1-956 <STO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 DIVLCTNKDIR-SKNTQYIVCNPGFWSLVRRIPLPLEQRASNK----FNSTGSIECLGER 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                BEKDKKFAV--IEDDSDEGGDDEYCDGDEDEDDLKKPLKLD-----ETDRFLMTLFF 681
                                                                                                                                            525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGQAWGTMMVHKGLDLPGLKIRNFVVVFKNNSTKKQYKKWVEL-----PITFPNLD 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELHELGIKSDWASGQKKSTASSADISASKQKQMEKLKMFADGENQILVSTSVAEEGLDI
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GKRFKALFMTPNSMILNQQETRISS-----YLTQTIQGSD--NVPTRNVIQSKDLIVA
                                                                                                                                                                          -----YEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTIRMIDAYTHLETFYN
                                                  TAQILENSLLNLENGEDAGVQ-----LSDFSLIIDECHHTNKEAVYNNIMRHYLMQK
                                                                             160 TPQMIVN-LCN-EHRDPLDDEXPPEQFFLSTFTIIFFDECHNIVKNSPYSNVMREY--HY
                                                                                                                                              LKNNRLKKENKPVIPLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENL
                                                                                                                                                                                                                                           DQLKNQIQEPCKKFAIADATREDP-----FKEKLLEIMTRIQTYCOMSPMSDFGTQP-
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12.1%; Score 642.5; DB 2; Length 956;
Best Local Similarity 25.0%; Pred. No. 4.7e-25;
Matches 253; Conservative 179; Mismatches 387; Indels 191
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A,Gene: C01B10.1
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30968
R;Blanchard, M.; Bradshaw, H.
Submitted to the EMBL Data Library, August 1999
A;Description: The sequence of C. elegans cosmid ColBlo..
A;Reference number: 220949
A;Accession: T30968
A;Accession: T30968
A;Accession: T30968
A;Accession: T30968
A;Canel type: DNA
A;Residues: 1-811 <BLA>
A;Accession: Bla <BLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCEAILCTSKDİR-SRNTQYLVCDPGFWSLVRKTRLTDEQQALİK----YNATGSİNCRR 947
                                                                                                                                                                                                                                                                                                                                                            623 VLKECFCTLSYNINFHPEVALNYLKDEM-----EY------RY-PNFTV 659
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                                                                                                                                                                                                                               QMSPMSDFGTQP-----YEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTIR
                                                                                                                                                                                                                                                                  Gaps
                                                                 456 NMPEGH---SLPQIIGLTASLGTGDKNDCLQVRNYTAGLCASMDVKDLSIVKDNLBELRG
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                                     LKKENKPVI PLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKN
                                                                                                                                                                MI-DAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLKKPLKLDETDRFLM
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A;Introns: 28/2; 58/1; 113/3; 135/3; 165/2; 208/1; 285/1; 320/1; 442/1;
A;Note: C01B10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
12.3%; Score 654; DB 2; Length 811;
Best Local Similarity 27.0%; Pred. No. 9.7e-26;
Matches 210; Conservative 147; Mismatches 318; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --CGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKW 1003
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Length 398;

Query Match
9.7%; Score 516; DB 2; Length 39:
Best Local Similarity 33.3%; Pred. No. 3.7e-19;
Matches 141; Conservative 68; Mismatches 157; Indels

648 GGDDEYCDGDEDDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNT 707

594 NRKERVC-----AEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDE 

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à 셤 ઠે -----DEIEODL-----TOR----PEEKLQELESVSRDPSNENPKLEDLCFI 708 IMEQYTRTEESARGIIFTKTRQSAYALSQWITENEK--FAEVGVKAHHLIGAGHSSEFKP

53

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MIQNEQKEVISKFR-TGKINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRAR 824

994 146

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884

885 KMKTKRNIAKHY--KNNPSLITFLCKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIVR 942 FIRDSOBKPKPVPDKENKKL---LCRKCKALACYTADVRVIBECHYTVLGDAFKECFVSR 318

1000 YKKW 1003 YSKW 381

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RESULT 5

206

262

825 ADESTYVLVAHSGSGVIEHETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEK

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C;Accession: T46312
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiema submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23036
A;Reference number: Z23036
A;Recession: T46312
A;Restous: preliminary
A;Molecule type: mRNA
A;Residues: 1.398 cAAA>
A;Cross-references: UNIRROT:O9NT04; EMBL:AL137608
A;Experimental source: adult testis; clone DKFZp434J1111
C;Genetics:
A;Note: DKFZp434J1111.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKAHHLIG---AGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVI 805
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                                                   LLVRDVL-----DKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSAF
                                                                      LNVLRQTGN-NELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
                                                                                                                                                                                 241 ENNSSESSFADSSVVSESDTSLA-EGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAAR
                                                                                                                                                                                                     222 IHIQRQFCLRNYQBELCQVALQGRNTIVTAPTGSGKTVIAANIIKEHFESR---SSEG--
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CESP: D
hypothetical protein D2005.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20332
R;Wilkinson, J
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19258
A;Reference number: Z19258
A;Recession: T20332
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1134 <WIL>
A;Residues: 1-1134 <WIL>
A;Cross-references: UNIPROT: Q93413; EMBL: Z79752; PIDN: CAB02082.1; GSPDB: GN00019; CESP: A;Genetics:
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Ge
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9.4%; Score 499; DB 2; Length 1134;
Best Local Similarity 23.5%; Pred. No. 1.2e-17;
Matches 193; Conservative 134; Mismatches 288; Indels 206;
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hypothetical protein DKF2p434J1111.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

RESULT 4

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A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0190
C;Superfamily: ATP-dependent RNA helicase eIF-4A
F;33-40/Region: nucleotide-binding motif A (P-loop) #status atypical
F;131-136/Region: DEAD/H motif
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D75219
ATP-dependent RNA helicase, eif-4a family PAB0190 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D75219
C;Accession: D75219
C;Accession: D75219
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struce and a prococcus abyssi genome sequence: insights into archaeal chromosome struce A;Accession: D75219
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9V1Z5; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB4920
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                                         404
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                                                                                 ---EVVKSCDIIISTAQILENSLINLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIM 458
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              ------ELQLRPYOMEVAQPALEGKNIIICLPTGSGKTRVAVY
                            IAKDHLDKKKKASEPGKVIVLVNKVLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFP
                                                                                                                                       RHYLMOKLKNNRLKKENKPVIPLPQILGLTASPG--VGGATKQAKAEBHILKLCANLDAF
                                                                                                                                                                                                                               517 TIKTV--KENLDQLKNQIQEPCKKFAIADATREDPFKE------KLLEIM----
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|KQTIQSVEPE------IVLRL-----KKYT--HQSVPHQFGNYGEQWVGY
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LKVIVATSVVEEGLDVTACNLIIKYNCSSGSAIQLVQQRGRARAKNSRSVLLSVK-SSIN
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probable ATP-dependent RNA helicase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
Cjate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: D71203
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekii
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                    LQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLV-N 364
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                                                                                                                                                                                                                                     KVLLVE--QLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKS---CDIIISTAQILEN
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                                                             Gaps
Query Match 8.5%; Score 453; DB 2; Length 752;
Best Local Similarity 25.3%; Pred. No. 1.5e-15;
Matches 183; Conservative 124; Mismatches 259; Indels 156;
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A;Cross-references: UNIPROT:059524; GB:AP000007; NID:g3236134; PIDN:BAA31019.1; PID:g325 A;Experimental source: strain 0T3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71203
A;Accession: D71203
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Residues: 1-650 <KAW>
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8.3%; Score 441.5; DB 2; Length
Best Local Similarity 25.9%; Pred. No. 4.6e-15;
Matches 185; Conservative 122; Mismatches 261; Indels
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RESULT 8 A69432 ATP-dependent RNA helicase homolog - Archaeoglobus fulgidus

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C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A64312
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
G;Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhout, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID: 98049343; PMID: 9389475
A;Accession: A64312
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Kesidues: 1-741 <KLES
A;Kesidues: 1-741 <KLES
A;Cross-references: UNIPROT: 028814; GB: AE001002; GB: AE000782; NID: 92689325; PIDN: AAB897
C;Superfamily: ATP-dependent RNA helicase eIF-4A
C;Superfamily: ATP-dependent RNA helicase eIF-4A
C;Superfamily: ATP-dependent RNA helicase eIF-4A
C;Superfamily: ATP-dependent RNA motif A (P-loop)
F;136-139/Region: nucleotide-binding motif B
F;136-139/Region: DEAD/H motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 VNKVLLVEQLFRKEFQPFLKKWYRV---IGLSGDTQLKISFPEVVKSCDIIISTAQILEN 419
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---PLILAMTASPG-----SDPERIMEVIQNLGIEAIEVRTEWDSDVAPYVGKKRIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 417; DB 1; Length 741 Best Local Similarity 23.8%; Pred. No. 9.9e-14; Matches 169; Conservative 114; Mismatches 230; Indels
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ETF-4A family probable ATP-dependent RNA helicase homolog - Methanococcus jannaschii CiSpecies: Methanococcus jannaschii CiSpecies: Methanococcus jannaschii CiSpecies: Methanococcus jannaschii CiDate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-May-2001 CiDate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-May-2001 CiDate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-May-2001 R.Putc. C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.Science 273, 1058-1073, 1996
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Aluthors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Reference number: A64300; MUID:96337999; PMID:868087
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--DEE-----LAIDRLKIFVED--WKNNKYSDNGPRIPVFD 337
                                                                N----EKLTKLRNTIMEQYTRIEESARGIIFTKTRQSAYALSQWITENEKFAEVGVKAHH 753
                                                                                                                                                                                                                                                                                                                                             812 NEIAMVOARGRARADESTYVLVAHSGSGVIE----HETVN-----DFREKMMYKAIHCV 861
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ERERVIDDIVYEVGETGALLTGLYAVSLLYNFCNTLSRDVYTRYYPTFTAQPCLSGWYCF 572
                                                                                                           754 LIGAGHS -- SEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGLVT
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                                                                                                                                                                                                                                                                                                                                                                                                              TVTQYVQSRGRARAMASKPLIFLNTEELLIHERILHEEKNLKFALSELSNSNIFDSLVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONMK-PEEYAHKILE-----LOMOSIMEKKMKT-KRNIAKHY----KNNPSLITFLC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (P-100p)
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A, Start codon: TTG
C, Supportamily: ATP-dependent RNA helicase eIF-4A
C, Keywords: ATP, nuclearide himain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Keywords: ATP; nucleotide binding; P-loop
F;41-48/Region: nucleotide-binding motif A (P
F;139-144/Region: nucleotide-binding motif B
F;413-146/Region: DEAH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVELPKACKVPAAQGSPAKSIRK 595
   KALGKOLSD-
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                                                                                                                                               pycobale R NA helicaese (Thomuclease SPACBA4.08c - fission yeast (Schizosaccharomyces pomb pycobale R NA helicaese (Thomuclease SPACBA4.08c - fission yeast (Schizosaccharomyces pomb C; Species: Schizosaccharomyces pomb C; Species: G-May-1996 Hesquence revision 13-Mar-1997 Hext_change 09-Jul-2004 C; Date: 16-May-1996 Hesquence revision 13-Mar-1997 Hext_change 09-Jul-2004 C; Accession: T39130; T41432; T4192; S6252, Rajandream, M.A.; Walsh, S.V. A; Reference number: Z21830 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T39130 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41432 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41444 A; Accession: T41
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                                                                                                                                        obable RNA helicase/ribonuclease SPAC8A4.08c - fission yeast (Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 ISTAQILENSLLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNR
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A;Map position: 3
F;32-39/Region: nucleotide-binding motif A (P-loop) #status atypical
F;141-146/Region: nucleotide-binding motif B
F;145-148/Region: DEAD/H motif #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.6%; Pred. No. 1.3e-12;
Matches 175; Conservative 107; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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	Qy 577PYEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQIND-TIRMID-AYTHLE 627		Db 366 ETFNPEFQKERM-KLEKAEHLSALIFVDQRYIAYSLLLMMRHIKSW 410 Qy 741 NEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGL 796	411	Qy 797 DIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIE 842  : :  :  :  :     :     :	QY 843 HETVNDFREKMMYKAIHCVQNMKPEBYAHKILELQMQSIMEKKMKRIAKRNIAKHYKNNP 900	Db 528 HNQIIPIEENGVIKYCABLLLPINSPIKHAIVLKNPMPNKKT 569 Ov 901 SLITFLCKNCSVIACSGR-DIHVIEKMHHVNMTPEPKR 937	: :	Qy 938 LYIVRENKALQKKCADY 954    :               Db 630 LYDKKIARALNESFVBADKECFIY 653	RESULT 12  E69055 ATP-dependent RNA helicase, eIF-4A family - Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 A; Smith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; A; Charch, G. M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J; Bacteriol. 179, 7135-7155, 1997 A; Tile Competie ganome sequence of Methanobacterium thermoautotrophicum Delta H. A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; Status; Dreliminary; nucleic acid sequence not shown; translation not shown A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; CGenetics: A; CGen
GTQPYEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTIRMIDAYTHLE 62	DD 307 KLSMQKTKSAKSIVNDE	IVIRY 80 :    YIIFY 43	QY 808 GLVTNEIAMVQARGRARADESTYYLVAHSGSGVIEHETVNDFREKMYKAIHCVQNM- 864	865KPEEYAHKILELQMQSIMEKKWKTKRNIAKHYKNNPSLITFLCKN 90	Db 496 YLLNKRLQKKFEEKSKEEIKEETEIKEKEIESKTAVKEETKEEEEKTKKPVTILDFIKQ 555 Qy 910 CSVLACSGEDIHVIEKMHHVNMTPEFKELYIVRE 943	Db 556 IEVKERSKSEEDKIKQEIKIPKKPIKIIVDVREKNMAKLLHNYANIELKTLEVGDYVLSD 615	QY         944 NKALQKKCADVQINGEI 960           1::   ::              Db         616 RVVVERKTAEDPVNSII 632	:	1485011 11 S4485011 11 K12H4.8 protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 30-Jun-2001	101.1; PID:g289703 ; 444/3; 512/2; 634/3; 694/3; 74 gth 1822; ndels 202; Gaps 37;LDKKKKASEPGKVIV 361   :

	Ov 306 LOLRPYOMEVAOPALEGKNIIICLPIGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK 365
Filo7-114/Region: nucleotide-binding motif A (F-to F;205-210/Region: nucleotide-binding motif B F:008-210/Region: DRBD/H motif	Best Local Similarity 21.6%; Pred. No. 2e-08; Matches 126; Conservative 91; Mismatches 190; Indels 175; Gaps 22;
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A;Cross-references: EMBL:X79743 A;Note: the nucleotide sequence was submitted to t C:Genetics:	A;Residues: 1-784 <sto></sto>
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Yeast 11, 61-78, 1995 A:Title: Nucleotide sequence and analysis of the c	Jung, A.H.; Aldm, M.; Fletcab, 1. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A.Murhors Hon. S. Daniela C. T. Dennis D. P. Omer. A.D.: Rhhardt. H.: Lowe. T.M.: Li
A; Kresidues: 1-993 <bad> A; Cross-references: UNIPROT: P40562; GB:Z47047; EMB R:VOSS H.: Tammanes: J.: Teodoru, C.; Valencia, A.</bad>	R,Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukka, H.D.; Lasky, S ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung V. H.; Maddocks, D.G.; Jablo
A;Accession: S48436 A;Molecule type: DNA	02-Feb-2001 #text_change 09-Jul-2004
submitted to the EMBL Data Library, August 1994 A;Reference number: S48432	4A [imported
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 C;Accession: 848435; S50885 R:Badcock, K.; Churcher, C.	RESULT 13
probable RNA helicase YIR002c - yeast (Saccharomyc N.Alternate names: hypothetical protein YIB2c	: :       : :
RESULT 14	12) NUNCOS VINA DE LINE CONTRACTOR DE LA
Db 437 AEEGLDVPEVDLVLFFEFVPTAIRSVQRKGRTGRQT	Qy 868 EYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSGEDIHVIEKMH 927
Qy 792 AEEGLDIKECNIVIRYGLVTNEIAWVQARGRARADE:	Db 447 EPVPSEIRMIQRRGRKRKGRMYVLITEKTRDEAYYXSSIRKERSMK-E 496
Db 384 EALTAFLGEHFDTRRFVGQGDADGSDGMT	QY 808 GLVTNEJAMVQARGRARADESTYVLVAHSGSGVJEHETVNDFREKMMYKALHCVQNMKPF 867
Qy 732 YALSOWITENEKFAEVGVKAHHLIGAGHSSEFKPMT	387 GINAVKFYGQNSRSGEKGLTQKQQRDIIKSFRMGNHDVLLSTSVAEEGIDIPSVDLVVWY
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Db 218ERVILPEEILEVRDAINDVIEDRLA	Qy 643 DDSDBGGDDEYCDGDEDEDDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPEY 696
Qy 590 AKKGNRKERVCAEHLRKYNBALQINDTIRMI DAY	Db 253 KDLLKARGRVQNRIARSTSPPRACYRAISLLASCINVEHALELLET 298
Db 203DA	Qy 588 KAAKKGNRKERVCAEHLRKYNEALQINDTIRMIDAYTHLFTFYNEEKDKKFAVIE 642
Qy 533 QEPCKKFAIADATREDPFKEKLLEIMTRIQTYCQMS	208
165	528 LKNQIQEPCKKFAIADATREDPFKEKLLEIMTRIQTYCQMSPMSDFGTQPYEQWAIQMEK
473 KENKPVIPLPQILGL	162HPLILGLTASPONDENT KTACCENLEMBEVOVKTEGDEDVRPYLKP
OY 413 IAQIIENSELNENGEENACHOSTELLEGENINGE Db 119 TPOVVENDLVGGRIDMDDVVHCTFDECHRA'	DD 117 TVESDILAGRYDLRDVSLIVFDECHRAVGSYSYVFLASNYIQNAK 161
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Qy 366 VLLVEQLFRKEFQPFLKKWYRVIGLSGI	DD 67 LSPSKPLAIQHEESFREFMLATCTSLTGSIKPEERKERWIKSQIISATPQ 116
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306 LOLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK 365

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4B. 238062; NID:g603997; PID:g763347; Misson, S.; Schwager, C.; Wiemann, S.; Schwager, C.;
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                                                          GETR-----PDDRRAAWTDARVVVA 118
                                                                                           TNKEAVYNNIMRHYLMOKLKNNRLK 472
                                                                                                                     ATGDYAYTYVAERYHAD----- 164
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DVGEHTHDTDVQW---- 217
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        EP-ELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIV 361
                             362 LVNKVLLVEQLFRKEFQPFLKKWYRVIGLSGDTQL--KISFPEVVKSC--DIIISTAQIL
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C;Species: Cenarchaeum symbiosum
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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Similarity 20.3%; Pred. No. 9e-08; Similarity 20.3%; Pred. No. 9e-08; Indels 197; Conservative 118; Mismatches 246; Indels 197
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK037057 Linear HTC 03-APR-200 MENA linear HTC 03-APR-200 Was musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930105804 product:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Home sapiens], full insert
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Sciurognathi; Muridae; Murinae; Mus
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similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5
similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5
[Homo sapiens] (SPTR [09H3G6, evidence: FASTY, 75.6%ID,
67.6%length, match=2079)"
/codon start=1
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QILKKINTCGNTSAAELLISTILGOGOWPLGWTOMPTALEHSGNPTARRYKFTITDL
PSPSSTAHDECLHLITLIQPTLVDKLLINDVLDTCFEKGLLITVEDRNRISAAGNSGN
ESGVRELIKRIVGVERMRSTFLDVLARQTGNDALFOELTGGGCPEDNTDLANSSHEDGP
AANECLLPAVDESSLETEAMNVDDILPEASCTDSSVTTESDTSLAEGSVSCFDESLGH
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By Adachi, J., Aizawa, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiroka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasai, C., Sakai, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Sh
rujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKKN integrated sequence analysis (RISA) system--384-format
Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2304)
                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase II Team and the
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db_xref="RANTOM DB:9930105B04"
/db_xref="reaxon:10090"
/clone="9930105B04"

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    /organism="Mus musculus"

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishil, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yondawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yongawa, T., Ozawa, K., Tamaka, T., Matsuura, S., Kawai, J., Nokazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                              AK040519

2331 bp mRNA linear HTC 03-APR-2004
Mus musculus 0 day neonate thymus CDNA, RIKEN full-length enriched
library, clone.4430105A06 product:similar to MELANOWA
DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens], full insert
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2331)

6 (bases 1 to 2331)

8 Adachi,J., Arizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagakk,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kondo,B., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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Sciurognathi, Muridae, Murinae, Mus
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   640 ValileGluAspAspSerAspGluGlyGlyAspAspGluTyrCysAspGlyAspGluAsp
                                                      GluaspaspleulyslysProleulysleuaspGluThraspargPheleuMetThrleu
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FUNCTIONAL annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOUGNAL Unpublished (1999)  COMMENT Email: cgapbe-r@mail.nih.gov Tissue Procurement: ATC CONDA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: MGC clone distribution DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at: http://image.llnl.gov Plate: LLAM12875 row: g column: 07 High quality sequence stop: 721. FRATURES Location/Qualifiers 1. 1013 /organism="Homo sapiens" // Mol_type="MRAB:5786526" // Lisue Lrype="MRAB:5786526" // L	Alignment Scores: 3.1e-160 Length: 1013 Pred. No.: 3.1e-160 Matches: 3.2 Score: 1597.00 Matches: 5 Percent Similarity: 94.15% Mismatches: 9 Query Match: 30.07% Indels: 8 DB: 5 US-09-515-363C-2 (1-1025) x BQ233683 (1-1013)	529 LysAsnGln11eGlnGluProCy	Db   122    CCAATGTCAGATTTGGAACTCAACCCTATGAACAATGGGCCATTCAAATGGAAAAAAA	649 GlyAspAspGluTyrCysAspGlyAspGluAspAspLeuLysLysProLeuLys
400 PheproGluvalValLysSerCysAapIleileileSerThrAlaGlnIleLeuGluAsn  1483 TTTCCAGAAGTTGTCAAATCTTACGATGTTATTATCAGCACTGCAAATCCTTGAAAAC  420 SerLeuLeuAsnLeuGluAsnGlyGluAspAlaGlyValGlnLeuSerAspPheSerLeu  1543 TCCCTCTTAAATCTGGAGAGGGAGGAGGCGGTGCGAGCTGCAGATTCTCTCTC	DD 1843 ACAGIGAAGGAATCTTGGTCAACTCAAACACCAAATAAGGAACCATGCAAGAATTT 1902  OY 540 AlailealaaspalaThrargGluaspProPheLysGluLysLeuLeuGluIleMetThr 559  1903 GTGATTGCTGATGACCAGAGAAATCCATTTAAAGAGAAACTTCTAGAATTATGGCA 1962  OY 560 ArgileGlnThrTyrCysGlnMetSerProMetSerAspPheGlyThrGlnProTyrGlu 579  1963 AGCATTCAGACTTCACCAAAAAGTCCCAATGTCAGATTTTGGAACCCAACATTATGAG 2022  OY 580 GINTTPALAILEGInMetGluLysLysAlaAlaLysLysGlyAsnArgLysGluArgYal 599	2023 CAGTGGGCCAAAGAAAAAAAAGACTGCTAAAGACGGAAATCGCAAAGATCGCGTC 600 CysAlaGluHisLeuArgLysTyrAsnGluAlaLeuGlnIleAsnAspThrIleArgMet 2083 TGTGCAGACATTTGAGGAAGTACAACGAAGCCCTACAAAATCAACGACGATCCGAATG 620 IleAspAlaTyrThrHisLeuGluThrPheTyrAsnGluGluLysAspLysLysPheAla 2143 ATTGATGCATATAGCCACCTGGAAGTTCTACACTGATGAGAAAGAA	Oy 640 ValileGluAspAspSerAspGluGlyGlyAspAspAspGluTyrCysAspGluAsp 659	BQ233683 BQ233683 LOCUS AGENCOURT 7258428 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5786526 5', mRNA Sequence. 5', mRNA Sequence. BQ233683 BQ233683.1 GI:20415083 KEYWORDS EST. ORGANISM Homo sapiens FURATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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AGENCOURT 8949486 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472264
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Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM14005 row: o column: 17
High quality sequence stop: 738.
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
           AsnGluGlnLysGluValIleSerLysPheArgThrGlyLysIleAsnLeuLeulleAla
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/clone="IMAGE:6472264"

/tiskue_type="leiomyosarcoma"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 1174)

S NIH-MGC http://mgc.nci.nih.gov/.

I (Date 1 1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapple-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 808.
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 HisTyrLeuMetGlnLysLeuLysAsnAsnArgLeuLysLysGluAsnLysProVallle 479
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Average insert size 2.1 kb. "
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BU189982
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Location/Qualifiers
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                                                                                                                            BU189982.1 GI:22703966
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1289.50
95.14%
93.40%
24.28%
                                                                                                                                                            Homo sapiens (human)
TCATAAGATT 851
                                                                                                                                                                               Homo sapiens
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Best Local Similarity:
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BM467983 1115 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6437921 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532884
5', mRNA Bequence.
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| Corganism="Homo sapiens"
| And Lype="mRNA"
| Ab Aref="taxon:9608"
| Clone="IMAGE:553884" |
| Clone="IMAGE:553884" |
| Clone="IMAGE:553884" |
| Clone="INAGE:573884" |
| Clone="Inb="NIH MGC 71" |
| Clone="Inb="NIH MGC 71" |
| Clone="Organ: uterus, Vector: pCMV-SPORT6; Site_1: Not1; |
| Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb.
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NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (WGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
High quality sequence stop: 690.
Location/Qualifiers
                                                                                                1115
228
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                                                                           286 hrMetGlySerAspSerAspGluGluAsnValAlaAlaArgAla
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1218.00
99.13%
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Homo sapiens
        278 erAsnMetGlySerAsp.
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Best Local Similarity:
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/note="Organ: uferus; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                                                                                                                                                                                                                                 MetSerAsnGlyTyrSerThrAspGluAsnPheArgTyrLeuIleSerCysPheArgAla
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Matches:
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Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.  Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."  Alignment Scores:	Qy         295 AsnValAlaArgAlaAserProGluProGluLeuGhLeuArgProTyrGlnWetGlu 314           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         355 GlubroGlyLy8VallleValLeuValAsnLy8ValLeuLeuValGluGlnLeuPheArg         374           Db         186 GAGCCTGGAAAGTTATAGTTCTTGTCAATAAGGTACTCCTAGTTGAACAGCTCTTCCGC         245           Qy         375 Ly8GluPheGlnProPheLeuLy8Ly8TrpTyTATGGTTATTGATTAGTGTATACCTGTTATTGC         394           Db         246 AAGGGTTCCAACCATTTTGAGAAATGGTATTGGTTATTGATTAAGTGGTATACC         305           Qy         395 GlnLeuLy81leSerPheProGluValValLy8SerCy8A8p1le1le1le1le1le1le1le1le1le1le1le1le1le1	Qy         435 SerAspPheSerLeuIleIleIleIleIleAspGluCysHisHisHisHisHisHanLysGluAlaValTyr 454           Db         426 TCAGACTTTCCCTCATTATCATGATGATGTCATCACCCACC	Qy 515 AlaPheThrIleLysThrValLysGluAsnLeuAspGlnLeuLysAsnGlnIleGlnGlu 534
	Oy 936 LysGluLeuTyrIleValArgGluAsnLysAlaLeuGlnLysLysCysAlaAspTyrGln 955	QY         996 ThrLysLysLysLysTrpValGluLeuProlleThrPheProAsnLeuAspTyr 1015           Db         601 ACAAAGAACAATACAAAAGTGGGTAGAATTACCTATCCCAATCTTGACTAT 660           QY         1016 SerGluCysCysLeuPheSerAspGluAsp 1025           Db         661 TCAGAATGCTGTTTATTAGTGATGAGGAT 690           RESULT 8         BF337464           LOCUS         BF337464           LOCUS         BF337464           ACCESSION         BF337464           S', mRNA sequence.           ACCESSION         BF337464           BF337464         GI:11283715	N H N H	http://image.llnl.gov Plate: LiaM949 be row: n column: 23 High quality sequence start: 5 High quality sequence stop: 695. Location/Qualifiers 1. 1035 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxNA" /

539

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BITOURS: LITERISSENCE

BETTOURS: LITERISSENCE

MUS musculus (house mouse)

MUS musculus (house mouse)

MUS musculus (house mouse)

MUS musculus (house mouse)

MUS musculus (house mouse)

MUS musculus (house mouse)

MUS musculus (house mouse)

BETTOURS: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CACABAI, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaddık, T. Tomaru, Y., Hasegawa, Y., Nogami, A.,

Kiyosawa, H., Yaddık, T. Tomaru, Y., Hall, D.P., Bult, C.,

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121 GCATTICIGAAIGITCTICGICAAACAGGAAACAAIGAACTIGICCAAGAGITAACAGGC 180
                                                                                                                                                                                            361 ACAAGITITGGCAGAAGGAAGIGICAGCIGCTIAGAIGAAAGICTIGGACATAACAGCAAC 420
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKKN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, Z., Yanagisawa, M., Yang, I., Yang, Z., Yang, Y., Zimener, A., Carninoi, P., Savolan, M., Zhu, Y., Zimer, A., Zimener, M., Carninoi, P., Sakazume, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, J., Alzawa, T., Kawai, J., Alzawa, K., Arakway, T., Eukuda, S., Hara, A., Hashizume, W., Imceni, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-45-503-922
Fax: 81-45-503-922
Email: genome-reedgec.riken.jp, URL:http://genome.gec.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nokamura,M.
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Obsato,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9130009C22"
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/dev_stage="adult"
/lab_host="DH108"
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DESTYVLVTSSGSGVTEREIVNDFREKMMYKAINRVQNMKPEEYAHKILELQVQSILE
KKKNYENSIA KAKYNDNPSLTTLLCKNCSMLVCSGENIHVIEKMHYNMTPEFKGLYIV
RENKALQKKFADYQTNGEIICKCGQAMGTMMVHKGLDLPCLKIRNFVNNFKNNSPKKQ
YKKWVELPIRFPDLDYSEYCLYSDED"
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_gtage="adult"
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Conservative:
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/db_xref="taxon:10090"
/clone="9130009C22"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/note="putative"
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

Nature 420, 563-573 (2002)

E (Dases 1 to 1197)

Radachi,J., Alazawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Hiramoto,K., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hiramoto,K., Timotani,K., Ishii,Y., Itoth,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Sano,H., Sasaki,D.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lease visit our web site (http://genome.gsc.riken.jp/) for further
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Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
        library, clone:9130009C22 product:similar to MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-5 [Homo sapiens], full insert
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Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                            Mus musculus (house mouse)
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COMMENT

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BE882040 1041 bp mRNA linear EST 20-OCT-2000 601505326F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906774 5',
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Drgan: uferus; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       ValGlnGluLeuThrGlySerAspCysSerGluSerAsnAlaGluIleGluAsnLeuSer
                                                                                                                            214 GlnValAspGlyProGlnValGluGluGlnLeuLeuSerThrThrValGlnProAsnLeu
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                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1170 row: 1 column: 22
High quality sequence stop: 731.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BX492926

DKF2P781C0628 rl 781 (synonym: hlcc4) Homo sapiens cDNA clone

DKF2P781C0628 s, mRNA sequence.

BX492926
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/note="vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
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                                                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumanlai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 627)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKZP); Email 8.wiemann@dKz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKZp781C028) is available at the RZPD in Berlin.
Please contact the RZDP. Reseourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
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        41
        368
        6.9
        864
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        QRF24
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        # ALIGNMENTS

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   . . ; IEA
  "mda-5: An interferon-inducible putative RNA helicase with double-
stranded RNA-dependent ATPase activity and melanoma growth-suppressive
   1 MSNGYSTDENFRYLISCFRARVÖMYIQVEPVLDYLFFLPAEVKEQIORTVATSCNMQAVE
   Gapa
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCPI_TaxID=9606;
  TISSUE-Melanoma;

Kang D.-C., Fisher P.B.;

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF095-844; AAG34368.1; --

HSSP; P10081; IFUK.

GO; GO:0008524; F:ATP binding; IEA.

GO; GO:0008056; F:ATP-dependent helicase activity; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0015668; F:type III site-specific deoxyribonuclease ac.

GO; GO:0009307; P:DNA restriction; IEA.
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  Length 1025;
   TIŜSUB=Melanoma;
MEDLINB=21664412; PubMed=11805321;
Kang D., Gopalkrishnan R.V., Wu Q., Jankowsky E., Pyle A.M.,
Fisher P.B.;
  InterPro; IPR01411; DEAD.
InterPro; IPR011029; DEATH like.
InterPro; IPR01059; Realingee_C.
InterPro; IPR005955; Realingee_C.
InterPro; IPR005915; Realingee_C, 1.
Pfam; PF0481; Resili; I.
SMART; SM00499; BELDC; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1025 AA; 116687 WW; 48BE75491D863741 CRC64;
  Indels
  01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Melanoma differentiation associated protein-5.
  100.0%; Score 5311; DB 2;
100.0%; Pred. No. 3.1e-256;
ive 0; Mismatches 0;
  Proc. Natl. Acad. Sci. U.S.A. 99:637-642(2002)
PRT; 1025 AA
   (TrEMBLrel. 16, Created)
   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
   Best Local Similarity 100.
Matches 1025; Conservative
PRELIMINARY;
   Homo sapiens (Human)
  Similarity
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  LQPTLVDKLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSA
   FLNVLRQTGNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
  FLAVERQTGNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
   LLLSTLEKGVWHLGWTREFVEALRRTGSPLAARYMNPELTDLPSPSFENAHDEYLQLLNL
  LOPTLVDKLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSA
   ENNSSESSFADSSVVSESDISLAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAARA
   SPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVI
  VLVNKVLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENS
   LINLENGEDAGVOLSDFSLIIIDECHHTNKEAVYNNIMRHYLMOKLKNNRLKKENKPVIP
  Gape
  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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  Length 1025;
   3; Indels
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA helicase-DEAD box protein RH116.
   Query Match 99.5%; Score 5285; DB 2; Best Local Similarity 99.5%; Pred. No. 6.1e-255; Matches 1020; Conservative 2; Mismatches 3;
   SEQUENCE FROM N.A.
  NCBI_TaxID=9606
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  601 AEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDE
   DDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESAR
   I EHETVNDFREKMYKAIHCVQNMKPEBYAHKILELQMQSIMEKKMKTKRNIAKHYKNNP
  SLITFLCKNCSVLACSGEDIHVIEKMHHVNMTBEFKELYIVRENKALQKKCADYQINGEI
   LQPTLVDKLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSA
  FINVLROTGNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
  PLNVLRQTGNNELVQELTGSDCSESNAEJENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
   241 ENNSSESSFADSSVVSESDTSLAEGSVSCLDESLGHNSNMGSDSGTMGSDSBEENVAARA
   SPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVI
  VLVNKVILVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENS
  LLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIP
   LINLENGEDAGVQLSDFSLIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIP
  LPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKKFA
   IADATREDPFKEKLLEIMTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKKGNRKERVC
  IADATREDPFKEKLLEIMTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKKGNRKERVC
   AEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDE
  DDLKKPLKLDETDRFLMTLFFENNKMLKRLAENPBYENEKLTKLRNTIMEQYTRTEESAR
   GIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRT
   GIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRT
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                                       LILISTLEKGVWHLGWTREFVEALRRTGSPLAARYMNPELTDLPSPSFENAHDEYLQLLNL
  LOPTLVDKLLVRDVLDKCMEBELLTIEDRNRIAAAENNGNESGVRELLKRIVQKENWFSA
  ENNSSESSFADSSVVSESDTSLAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAARA
  SPEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVI
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LPQILGLTASPGVGGATKQAKAEBHILKLCANLDAFTIKTVKENLDQLKXQIQEPCKKFA 540

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PRELIMINARY;

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Length 1025;

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   PLPQILGLTASPGVGAAKKQSEAEKHILNICANLDAFTIKTVKENLGQLKHQIKEPCKKF
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   541 VIADDTRENPFKEKLLEIMASIQTYCQKSPMSDFGTQHYEQWAIQMEKKAAKDGNRKDRV
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  RGIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFR
   TGKINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSG
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  VTEREIVNDFREKAMYKAINRVONMKPEEYAHKILELOVOSILEKKAKVKRSIAKOYNDN
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Rovacsovics M., Martinon F., Micheau O., Bodmer J.L., Hofmann K.,

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Created)
Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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960 IICKCGQAMGTMAVHKGLDLPCLKIRNFVVNFKNNSPKKQYKKWVELPIRFPDLDYSEYC 1019
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  Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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  600 CAEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDED
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Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  Xang D.-C., Fisher P.B.;

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X Kang D.-C., Fisher P.B.;

X Submitted (Ash 2001) to the EMBL/GenBank/DDBJ databases.

X Submitted (Ash 2001) to the EMBL/GenBank/DDBJ databases.

X EMBL; AFR 2001) to the EMBL/GenBank/DDBJ databases.

X EMBL; AFR 2001 to the EMBL/GenBank/DDBJ databases.

X GO; GO:0008026; F:ATP binding; IEA.

X GO; GO:0008026; F:ATP dependent helicase activity; IEA.

X GO; GO:0003676; F:ATP-dependent helicase activity; IEA.

X GO; GO:0003037 p:DNB restriction; IEA.

X GO; GO:0003037 p:DNB restriction; IEA.

X GO; GO:0003037 p:DNB restriction; IEA.

X GO; CO:0003037 p:DNB restriction; IEA.

X GO; CO:0003037 p:DNB restriction; IEA.

X InterPro; IPR001629; Helicase_C.

X InterPro; IPR006935; ResIII.

X RART; SM00497; Helicase; Hydrolase.

X SART; SM00490; Helicase; Hydrolase.

X ATP-binding; Helicase; Hydrolase.
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  1 MSIVCSAEDSFRNLILFFRPRLKMYIQVEPVLDHLIFLSAETKEQILKKINTCGNTSAAE
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   LQPTLVDKLLVRDVLDKCMEEELLT1EDRNR1AAAENNGNESGVRELLKR1VQKENWFSA
   FLNVLROTGNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
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   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
Melanoma differentiation associated gene 5-like protein.
Name=9130099C22Rik;
Nus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Muscularia; LaxID=10090;
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human
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   Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078180; AAH78180.1; -.
  Length
   DE35A4B7D4B70EBC CRC64;
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
  7
   Score 3954; DB 2
Pred. No. 9e-189;
  3; Mismatches
  772 AA; 87604 MW;
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  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult female vagina cDNA, RIKEN full-length enriched
library, clone:9930105804 product:similar to MELANOWA DIFFERENTIATION
ASSOCIATED PROTEIN-5 (Fragment).
  SEQUENCE FROM N.A.
STRAIN=CSTBL/6J; TISSUE=Vagina;
STRAIN=CSTBL/6J; TISSUE=Vagina;
The PANTOM CORSOLTLUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
  MEDLINE-20530913; PubMed=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii W., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Foreda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika Sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10:1617-1630 (2000).
  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
N.S. TaxiD=10090;
                                   721 GIIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQKKKK 772
   "Functional annotation of a full-length mouse cDNA collection.";
   STRAIN=CS7BL/6J; TISSUE=Vagina;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Haysshida K., Hayatu N., Hiramoto K., Hiracka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
  GIIFTKTROSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQK
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STRAIN-CSTBL/60; TISSUE-Vagina;
MEDILINE-21085660; Pubmed-11217851;
RIKEN FANTOM CONSORTIUM;
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STRAIN=C57BL/6J; TISSUE=Vagina;
MEDLINE=20499374; PubMed=11042159;
   STRAIN=C57BL/6J; TISSUE=Vagina;
MEDLINE=99279253; PubMed=10349636;
  Carninci P., Hayashizaki Y.,
"High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
  Nature 409:685-690(2001).
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
721
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Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nahi K., Numara K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito H., Saito H., Sakai C., Sakai K., Sakazume N., Sano H., Saito H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Lubmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Bubi, AK037057; BAC25687.1; ---
Bubi, MGJ; MGJ; Bill Falt P. Dinding; IEA.

GO; GO:0008026; F:ATP-dependent helicase activity; IEA.

GO; GO:0008026; F:ATP-dependent helicase activity; IEA.

GO; GO:00090797; P:DNA restriction; IEA.

GO; GO:00090307; P:DNA restriction; IEA.

InterPro; IPR001410; DEAD.

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InterPro; IPR006935; ResIII.

Brim; PF0481; ResIII.

SR SMART; SM0487; DEADC; 1.
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  181 FLNVLRQTGNNELVQELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGM
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Thymus;
X MEDIANE=20530913; PubMed=11076861;
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nashinc T., Tashiro H., Itoh M., Azawa K., Mazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Ishikawa T., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
   SEQUENCE FROM N.A.
STRAINE-CYBHL/GJ; IISSUE=Thymus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
   STRAIN-C57BL/61; IISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
  01-WAR-2003 (TrEMBLE). 23, Last sequence update)
01-WAR-2004 (TrEMBLE). 26, Last annotation update)
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430105A06 product:similar to MELANOMA DIFFERENTIATION
ASSOCIATED PROTEIN-5 (Fragment).
   ŝ
   SEQUENCE FROM N.A.

STRAIN-CSTBL/GJ; TISSUE=Thymus;

Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T.,

Hayashida K., Hayateu N., Hiramoko K., Hiraoka T.,

Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Ś

Kutihara C., Maelauyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  collection.";
  CDNA
  "Functional annotation of a full-length mouse Nature 409:685-690(2001).
   cDNA cloning.";
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683
   Created)
PRT;
  SEQUENCE FROM N.A.
STRAIN=C77BL/61; TISSUE-Thymus;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA ometh. Enzymol. 303:19-44(1999).
  SEQUENCE FROM N.A.
STRAIN-CSPBL/6J, TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM COMSORTIUM;
   (TrEMBLrel. 23,
   Name=9130009C22Rik;
Mus musculus (Mouse).
  SEQUENCE FROM N.A.
   NCBI_TaxID=10090;
   01-MAR-2003
    QBBYC9
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CDNAB."
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  CAEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDED 659
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  .; IEA
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK040519; BAC30614.1;

R MGD; MGI:1918836; 91300095C2ZRik.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:000554; F:ATP dependent helicase activity; IEA.

R GO; GO:000366; F:ATP-dependent helicase activity; IEA.

R GO; GO:000307; P:DNA restriction; IEA.

R GO; GO:000307; P:DNA restriction; IEA.

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R InterPro; IRR006935; ResIII.

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   541 VIADDTRENPFKEKLLEIMASIQTYCOKSPMSDFGTOHYEOWAIOMEKKAAKDGNRKDRV
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RESULT Q96MX8

PARAGEMENT OLOURY:

RA OLE T., SUZUKLY.

RA OLE T., SUZUKLY.

RA WAKAMARICA N., NISHIKAWA T., OLSUKLY.

RA WAKAMARICA N., MAYABAH K., SACO H., NABAMAR T., TENBKE T., ISHIS S.

RA YAMMAROL J., SAILO K., KAWAI Y., ISONO Y., NAKAMURA T., ISHIS S.

RA WAKAMARI K., YASUGA T., WAYAMARI T., WAGABURA R., NAGAMARI K., YASUGA Y., WAYAMAR M., YOKOI T., FULVYA T., KIKKAWA E., OMURA Y.,

RA Abe K., KAMINARA K., YOKOI T., PULVYA T., KIKKAWA E., OMURA Y.,

RA Abe K., KAMINARA K., YOKOI T., PULVYA T., KIKKAWA E., ISHIGA S.,

RA TAMAHASHI M., WALANDA M., SALO K., TANIKAWA K., FUJIMORI K.,

RA ADONIYA K., ISHIDASHI T., YAMASHILA H., MURAKAWA K., FUJIMORI K.,

RA ADONIYA K., TAKABASHI-FUJII A., HARA H., TANBSE T., NOMURA Y.,

RA KANADORI K., TAKABASHI-FUJII A., HARA H., TANBSE T., NOMURA Y.,

RA KANADORI K., MALSUNAWA H., ICHINARA T., SHIOHATA N., SANO S.,

RA YOSHIKAWA Y., MALSUNAWA H., ICHINARA T., SHIOHATA N., SANO S.,

NOMIYAS S., MOMIYAMA H., SALON N., TAKAMI S., TERSHIMA Y., SALON N.,

RA HIBHIGAKI H., WALANDE K., KUMAGAI A., ILAKURA S., FUKUZUMI Y.,

RA YAMAZAKI M., WALANDE K., KUMAGAI A., ILAKURA S., FUKUZUMI Y.,

RA YAMAZAKI M., WALANDE K., KUMAGAI A., ILAKURA S., FUKUZUMI Y.,

RA YAMAZAKI M., WALANDE K., KUMAGAI A., ILAKURA S., FUKUZUMI Y.,

RA YUMALA S., NOMIYAMA M., TASHINO M., OHMORI Y.,

RA KAWADATA A., HIKIJI T., KODATAKE N., INAGAMA M., OHMORI Y.,

RA HIRIJAMA H., NOWONI S., ILON T., SARGAKI M.,

RA YOSHIMIRA K., NAKAMA T., NOWONI S., ILON T., SARGAKI M.,

RA TOGASHI T., OYAMA M., HATA H., WATANADE M., KOMASHI T., NOWUMA S., NOWUMAR Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMAN Y., NARAMA ö 677 738 ITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLD 797 9 RMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLKKPLKLDETDRFLM TLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIFTKTRQSAYALSQW 558 MTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTI 1 MTRIQTYCQMSPMSDFGTQPYEQWAIQMEKKAAKEGNRKERVCAEHLRKYNEALQINDTI Gaps Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ö 46.2%; Score 2456; DB 2; Length 468; 99.1%; Pred. No. 2e-114; live 2; Mismatches 2; Indels ( GO; GO:000554; F:ATP binding; IEA.
GO; GO:000526; F:ATP-dependent helicase activity; IEA.
GO; GO:0003076; F:Nucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001450; Helicase\_C. 468 AA; 54470 MW; 33D4D055C7436DFA CRC64; 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Created) Hypothetical protein FLJ31731. Homo sapiens (Human). Nat. Genet. 36:40-45(2004). EMBL; AK056293; BAB71141.1; -. HSSP; P10081; 1FUK. , Helicase C; 1. SMART; SM00490; HELICC; 1. 464; Conservative PRELIMINARY; Similarity SEQUENCE FROM N.A. NCBI\_TaxID=9606; PubMed=14702039; Helicase. Query Match Best Local S Matches 464 618 SEQUENCE 61 678 Match 유

750

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Gaps

1; 514;

DB 2; Length

Pred. No. 3.7e-105;

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  1 ANLDAFTIKTVKENLGQLKHQIXEPCKKFVIADDTRENPFKEKLLEIMASIQTYCQKSPM
  61 SDFGTQHYEQWAIQMEKKAAKDGNRKDRVCAEHLRKYNEALQINDTIRMIDAYSHLETFY
  AENPEYENEKLTKLRNTIMEQYTRTEESARGIIFTKTROSAYALSQWITENEKFAEVGVK
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   571 SDFGTQPYEQWAIQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTIRMIDAYTHLETFY
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85.0%; Pred. No. 3.7e
ive 30; Mismatches
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  TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XX TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XIAUSHORE, R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeperg H.B., Parmer T., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malany S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malank J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
  917
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   420
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301 IHCVQNMKPBEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSG
   EDIHVIEKMHUNMTPEFKELYIVRENKTLQKKCADYQINGEIICKCGQAMGTMMVHKGL
   IHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSG
   EDIHVIEKMHHVNMTPEFKELYIVRENKALQKKCADYQINGEIICKCGQAWGTMMVHKGL
  IKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKMMYKA
  STRAIN-CZECH II;
TISSUE-Mammary tumor metaatatized to lung. Tumor aroae spontaneously;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
  DLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED 1025
  Straubberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040313, AA4004031.1; -.
MGD; MGI:1918836; 91300905222Rik.
GG); GG:0008026; F:ATP binding; IEA.
GG); GG:0008026; F:ATP-dependent helicase activity; IEA.
GG); GG:0003676; F:Nucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR01650; Helicase_C.
Ffam; PF00271; Helicase_C: 1.
   DLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
  Last sequence update)
Last annotation update)
  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
  Created)
  099KS4;
01-JUN-2001 (TrEMBLrel. 17;
01-JUN-2001 (TrEMBLrel. 17;
01-MAR-2004 (TrEMBLrel. 26;
   Ifihl protein (Fragment).
Name=Ifihl;
   PRELIMINARY;
   Mus musculus (Mouse)
   SEQUENCE FROM N.A.
  [1]
SEQUENCE FROM N.A.
   STRAIN=CZECH II;
   828
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STRANDEMIX FVB/N;
C TISSUE-Amamary tumor. WAP-TGF alpha model. 7 months old;
X REDLINE=22388257; bubbmed=1247932;
X RIAUBERT E.D.; Feingold E.A.; Grouse L.H.; Derge J.G.;
X Klausher R.D.; Collins F.S.; Wagner L.; Schemen C.M.; Schuler G.D.;
A Klausher R.D.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
A Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
A Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.; Scheetz T.E.;
A Brownstein M.J.; Judin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;
Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
A Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
A Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus
Created)
Last sequence update)
Last annotation update)
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
  MEDLINE=22341132; PubMed=12454917;
  Dev. Dyn. 225:384-391(2002)
   mouse cDNA sequences."
                          Xenopodinae; Xenopus.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
                                   NCBI_TaxID=8355;
  TISSUE=Spleen;
  TISSUE=Spleen;
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   857
  240 IKECNIVIRYGLVINEIAMVQARGRARADESTYVLVISSGSGVTEREIVNDFREKMYKA 299
   917
  359
   977
  419
  9
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
  120 NLFFDNKKMLKKLAENPKYENEKLIKLRNTILEQFTRSEBSSRGIIFTKTRQSTYALSQW
   MTRIQTYCQMSPMSDFGTQPYEQWAlQMEKKAAKKGNRKERVCAEHLRKYNEALQINDTI
   RMIDAYTHLETFYNEEXDKKFAVIEDDSDEGGDDEYCDGDEDDDLKKPLKLDETDRFLM
   TLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIFTKTRQSAYALSQW
  738 ITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKINLLIATTVAEEGLD
   798 IKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKMMYKA
   IHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLITFLCKNCSVLACSG
  EDIHVIEKMHHVNMTPEFKELYIVRENKALQKKCADYQINGEIICKCGQAWGTMMVHKGL
  MASIQTYCOKSPMSDFGTQHYEQWAIQMEKKAAKDGNRKDRVCAEHLRKYNEALQINDTI
   Gaps
  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   1;
   DB 2; Length 467;
  DLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED 1025
  ; Score 2059.5; DB 2; Length
; Pred. No. 1.2e-94;
28; Mismatches 43; Indels
  Submitted (NAR-2002) to the EMBL/GenBank/DDBJ databages.
EMBL; BC025508; AAH25508.1; -.
MGD; MGI:1918836; 9130009C22Rik.
GO; GO:0005524; FATP binding; IEA.
GO; GO:000556; FATP binding; IEA.
GO; GO:0005676; F:ATP binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Ffam; PF00211; Helicase_C; 1.
SWART; SM00490; HELICC; 1.
   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
   53965 MW; F3B0D976778F0442 CRC64;
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
  682 AA
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84.6%;
   Matches 396; Conservative
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   Local Similarity
  SEQUENCE FROM N.A.
  STRAIN=Mix FVB/N;
  Strausberg R.
   61
   678
   858
  360
   618
  978
   420
  Query Match
  Q6GNI3
Q6GNI3;
  RESULT 11
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REC TISSUE=59leen;

REC TISSUE=59leen;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Fearbard L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Norlay M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human
   306 LOLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK 365
  366 VLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLE 425
  GLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKKFAIADAT 545
   426 NGEDAGVQLSDFSLIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIPLPQIL
  Gарв
  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
  50,
  Length 682;
  Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073528; AAH73528.1; -
InterPro; IPR011545; DEAD, DEAH. N.
InterPro; IPR011545; DEAD/DEAH. N.
InterPro; IPR001563; ResIII.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF04851; ResIII; 1.
SMART; SM00487; DEXDC; 1.
  Query Match
28.3%; Score 1505; DB 2; Length 6|
Best Local Similarity 43.9%; Pred. No. 8.8e-67;
Matches 313; Conservative 128; Mismatches 222; Indels
   ATP-binding, Helicase, Hydrolase, Hypothetical protein.
SEQUENCE 682 AA, 79244 MW, 5BF182DB298BCC4C CRC64;
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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615
REDPFKEKLLEIMTRIQTYCQMSPM--SDFGTQPYEQWAIQMEKKAAKKGNRKERVCAEH 603
  723
   783
   435
  784 NLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEH 843
  495
  903
   555
   904 TFLCKNCSVLACSGEDIHVIEKWHHVNMTPEFKELY-IVRENKALQKKCADYQINGEIIC 962
   DECURBER FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE=2234683; PubMed=12466851; DOI=10.1038/nature01266;

NA CAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

NA MAGARIN A., Maston R., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Harapin A., Matsuda H., Batalov S., Baisel K.W.,

Baldarelli R., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

A Gasterfland T., Gariboldi M., Gissi C., Godzik A., Gousins S.,

A Gasterfland T., Gariboldi M., Gissi C., Godzik A., Grusins S.,

A Grimmond S., Gustincich S., Hirokawa N., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RAGIGHA A., Kucokhkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pertea G., Pescole G.,

Petroveky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
   ŝ
                     -----DPTDAFLIQLFDGNRARLIELAQDVRFENPKLRKLEBILRDQF-QFSSGSRGII
  ETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPSLI
   LRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDDDL
  664 KKPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGII
   FTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKI
  MEDLINE=21100887; PubMed=11161808; DOI=10.1006/geno.2000.6433; Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T., Dewar K., Hennighausen L.; "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
  099JB7; 09D1X4;
01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Probable ATP-dependent helicase LGP2 (EC 3.6.1.-) (Protein D11Lgp2)
  KCGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDY 1015
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SEQUENCE FROM N.A. (ISOFORM 1).
   Name=Lgp2; Synonyms=D111gp2e;
Mus musculus (Mouse).
   zebrafish to mouse.";
Genomics 71:150-155(2001).
  STANDARD;
  NCBI_TaxID=10090;
  LGP2 MOUSE
  844
  286
  323
   724
   376
   496
   604
   RESULT 12
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Ransair T. Read JC., Read D.J., Raid G. T., Strong R. S., Ringwald M., Sandalin. A. Schneider C. G. Senpie C. A., Setcu M., Shinada K., Nelson R. Y., Taylor M. S., Tesedale R. D., Tomita M., Wells S. M. Vezardo. B. W. Vezardo. B. M. T. Taylor M. S., Tesedale R. D., Tomita M., Wells S. M. Vezardo. B. M. Vezardo. B. M. Vezardo. B. M. Vezardo. B. M. Sandalin. S. M. Vezardo. B. M. Shinagawa M., Wangara I., Wells S. M. Shinagawa M., Wangara I., M. Hara A., Hankizaka T., Komito M., Markarda M. Sandalin. San
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678 AA

STANDARD;

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365
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   373
  845 TVNDFREKAMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKAMKTKRNIAKHYKNNPSLIT 904
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   668
   306 LQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK
   VLLVEQLFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLE
   426 NGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIPLPOIL
   --EDEHVELREFSLIVVDECHHTHKDTVYNTILSRYLEQKLK----KAE----PLPQVL
   GLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKKFAIADAT
   REDPFKEKLLEIMTRIQTYCQMSPM-SDFGTQPYEQWAIQMEKKAAKKGNRKERVCAEHL
   RKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGGDDEYCDGDEDDDLK
  665 KPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIF
   TKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEQKEVISKFRTGKIN
   LLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHE
EMBL; BC0292U9; ATLEGOS.
MGD; MGI:1931560; DILEGOS.
INTERPRO; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR001450; Helicase_C.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00487; DEXDC; 1.
Alternative splicing; ATP-binding; Coiled coil; Helicase; Hydrolase.
The standard of the splicing; ATP-binding; Coiled coil; Helicase; Hydrolase.
The standard of the splicing; ATP-binding; Coiled coil; Helicase; Hydrolase.
The standard of the splicing; ATP-binding; Coiled coil; Helicase; Hydrolase.
  Gaps
   614 NCGEVWGFQMIYKSVTLPVLKIGS--MLLETPRGKIQAKKWSRVPFSIPVFDILQDC
  52;
  DB 1; Length 678;
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LC -> VS (in isoform 2).
/FTId-VSP 010842.
Missing (in isoform 2).
/FTIG-VSP 010843.
   (in isoform 2).
   Score 1356; DB 1,
NO. 2.3e-59;
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  25.5%;
   190
   678 AA;
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188
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  434
   905
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   605
   285
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LGP2\_HUMAN RESULT 13

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TISSUE=Colon; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnss.242603899; IISSUE=Embryo; PubMed=14702039; DOI=10.1038/ng1285; homolog).
Name=LGP2; Synonyms=D11LGP2E; Genet. 36:40-45(2004). SEQUENCE FROM N.A. SEQUENCE FROM N.A. 

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  433
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   LOLRPYOMEVAOPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIVLVNK 365
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  NGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPVIPLPQIL 485
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   RKYNBALQINDTIRMIDAYTHLETFYNBEKDKKFAVIEDDSDEGGDDEYCDGDEDEDDLK
   546 REDPFKEKLLEIMTRIQTYCOMSPMS-DFGTOPYEOWAIOMEKKAAKKGNRKERVCAEHL
  RRYNDALLIHDTVRAVDALAALQDFYHREHVTKTQIL---------------
   KPLKLDETDRFLMTLFFENNKMLKRLAENPEYENEKLTKLRNTIMEQYTRTEESARGIIF
  -----AERRLLALFDDRKNELAHLATHGP-ENPKLEMLEKILOROFS-SSNSPRGIIF
  TKTROSAYALSOWITENEKFAEVGVKAHHLIGAGHSSEFKPMTQNEOKEVISKFRTGKIN
  LLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVIEHE
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Best Local Similarity 40.7%; Pred. No. 3.7e-59;
Matches 292; Conservative 136; Mismatches 237; Indels 52
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  ATP (Potential).
DECH box.
Colled coil (Potential).
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R -> Q (in dbSNP:2074160).
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R -> W (in Ref. 1).
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MIM; 608588; -...
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InterPro; 1PR0010560; Helicase_C.
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SMART; SM00480; HELICG; 1.
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ATP-binding; Coiled coil; Helicas
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FLCKNCSVLACSGEDIHVIEKWHHVNMTPEFKELY-IVRENKALQKKCADYQINGEIICK 963
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum;
STRAIN=C57BL/6J; TISSUE=Cecum;
STRAIN=C57BL/6J; TISSUE=Cecum;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa M., Nishine T., Harda A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harda A., Amamence R., Matsumcto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Okazaki Y., Miramatsu M., Inoue Y., Kira A., Hayashizaki Y., Gramat Pair RIKEN integrated sequence N., Rira A., Hayashizaki Y., Genome Res. 10:1757-1771(2000).
  MEDILINE=20499374; PubMed=110042159; Carninci P., Shibata K., Itoh M., Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayathizaki Y., "Nuramatsu M., Hayathizaki Y., prispiration of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
   -CGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECC 1019
  ğ
  enriched
DIFFERENTIATION
  STRAIN-C57BL/60; TISSUB-Cecum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
[60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
   614 NCGEVWGLQMIYKSVKLPVLKVRS--MLETPQGRIQAKKWSRVPFSVPDPDFLQHC
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
  'Punctional annotation of a full-length mouse cDNA collection.";
   01-UTN-2001 (TrEMBLrel. 17, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male cecum cDNA, RIKEN full-length
library, clone:9130009C22 product:similar to MELANOWA
Name=9130009C22Rik;
  STRAIN=CSTBL/66; TISSUE=Cecum;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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STRAIN=C78HL/60; TISSUE=Cecum;
STRAIN=C78HL/60; TISSUE=11217851;
RIKEN FANTOM CONSORTIUM;
   SEQUENCE FROM N.A.
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   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum;
   Nature 409:685-690(2001).
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
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AC Q9D2Z5;
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70 VWHLGWTREFVEALRRTGSPLAARYMNPELTDLPSPSFENAH--DEYLQLLNLLQPTLVD 127
  128 KLLVRDVLDKCMEEELLTIEDRNRIAAAENNGNESGVRELLKRIVQ--KENWFSAFLNVL 185
  362 LVNKVLLVEQ----LFRKEFQPFLKKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILE 418
   NSLLNLENGEDAGVQLSDFSLIIIDECHHTNKEAVYNNIMRHYLMQKLKNNRLKKENKPV 478
   PEPELQLRPYQMEVAQPALEGKNIIICLPTGSGKTRVAVYIAKDHLDKKKKASEPGKVIV 361
   FAIADATREDPFKE------KLLEIMTRIGTYCOMSPMSDFGTQPYEOW 581
   AIQMEKKA----AKKGNRKERVC----AEHLRKYNEALQINDTIRMIDAYTHLETFYN 631
   12 RYLISCFRARVKMYIQVEPVLDYLT--FLPAEVKEQIQRTVATSGNMQAVELLLSTLEKG
  186 ROTGNNELVOELTGSDCSESNAEIENLSQVDGPQVEEQLLSTTVQPNLEKEVWGMEN---
   -NSSESSFADSSVVSESDTSLAEGSVSCLDESLGHNSNMGSDSGTMGSDSDEENVAARAS
  220 ONLSENSCPPSEV---SDTNL-----YS
   479 IPLPQILGLTASPGVGGATKQAKAEEHILKLCANLDAFTIKTVKENLDQLKNQIQEPCKK
  EEKDKKFAVIEDDSDEGGDDEYCDGDEDDDLKKPLKLDETDRFLMTLFFENNKMLKRLA
   573 NVRAAGFEEIEQD------LTQRFEEKLQELESVS
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GO; GO:000366; F:ATP-dependent helicase activity; IEA.
GO; GO:0000166; F:nucleic acid binding; IEA.
R InterPro; IPR001359; AAA ATPase.
R InterPro; IPR001410; DEAD.
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R InterPro; IPR011650; Helicase.
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R Ffam; PF00270; DEAD; 1.
R SWART; SW00487; DEXD; 1.
R SWART; SW00487; DEXD; 1.
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R SWART; SW00490; HELICC; 1.
R SWART; SW00490; HELICC; 1.
R SWART; SW00490; HELICC; 1.
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   962 CKCGQAWGTMMVHKGLDLPCLKIRNFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLF 1021
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   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoco K., Hiracka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Kohon H., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
   782 KINLLIATTVAEEGLDIKECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGSGVI
  EHETVNDFREKMMYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYKNNPS
   Gaps
   Sun Y.W.; "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic acid during the differentiation of acute promyelocytic leukemia cell.";
   Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
   ;
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  Yi-Wu S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
  MGD; MGT:1918836; 9130009022Rik.
MGD; GO:000524; F:ATP binding; IEA.
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InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
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Last sequence update)
Last annotation update)
   21.1%; Score 1122; DB 2;
88.1%; Pred. No. 2.5e-48;
iive 11; Mismatches 18;
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Pfam; PF00271; Helicase_C; 1.
NON TER 1
  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
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   Homo sapiens (Human)
  Similarity
   1022 SDED 1025
  [1]
SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  241 SDED 244
  NCBI TaxID=9606;
  RNA helicase.
   Name=RIG-I;
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